

QY 325 FQKEWHIQDYENYAPGYNDKIWGYDDLASISCKLAFKLKELGVSVMVMSLENDDEFK 384
Db 288 FLKNGATQGWDAQEVYAYQGNVWVYDNIKSFIDIKAOGLKFNKFGGAMVMAIDLDLDDFT 347
QY 385 G-HCGP-KNPLLNKVNHNMGDEKNSPECILGPGSTTTPTTTPTTTPTTTPTTTPS 437
Db 348 GTFNCGKFFLI-----STLKKALGLQSASCTAPAOPIEPIITAAPSGS 390

RESULT 15

US-10-004-219B-1
; Sequence 1, Application US/10004219B
; Publication No. US2003008741A1
; GENERAL INFORMATION:
; APPLICANT: Macrozyme
; APPLICANT: Aerts, Johannes M.F.G.
; APPLICANT: Boot, Rolf G.
; TITLE OF INVENTION: A mammalian mucinase, its recombinant production, and
; TITLE OF INVENTION: its use in therapy or prophylaxis against diseases in
; TITLE OF INVENTION: which mucus is involved or infection diseases
; FILE REFERENCE: 2183-5136US
; CURRENT APPLICATION NUMBER: US/10/004,219B
; CURRENT FILING DATE: 2001-11-02
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 1
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: human AMCase
; OTHER INFORMATION: amino acid sequence deduced from cDNA sequence
US-10-004-219B-1

Query Match 22.8%; Score 708.5; DB 14; Length 476;
Best Local Similarity 35.9%; Pred. No. 8.6e-44;
Matches 149; Conservative 75; Mismatches 154; Indels 37; Gaps 10;
QY 34 RIVCYVGTWVYHK-VDPYTIEDIDPFKCTHMYGPAKIDIEYKVTIQVDFPYQDDNHSW 92
Db 23 QTCYFTNWQYRGLEGRFMDNIDPCLCTHLYAFAGRONNEIT-----IEW 71
QY 93 -EKGYERFNNRLKNPETLMTISLGGVYEGSEKYSDMAANPTVQQFIOVLDFLQYK 151
Db 72 NDVTLQAFNGLKKNKSQLKTLAIGGNFTGAPFTAMVSTPENRQTFITSVIKFLRQYE 131
QY 152 FDGLDLWEYVPGSLGNPKIDKQNYLALVRELKDAFEPHG-----YLLTAAVSPGKDK 204
Db 132 FDGLDFWEYVPGSR-GSPFQDQKHLFTLVQEMREAPQEAQINKPRLMVTAAAGISN 190
QY 205 IDRAYDIKELNKLFDWNVMTYDHYGWNIFYGHNAPLYKRPDETDELHTYFNVNYTMHY 264
Db 191 IQSGYEIPQLSQYLDYTHVMYDYLHGSWEGYTGENSEPLYKYPTDTGS-NAYLNVYVMNY 249
QY 265 YLNNGATRDKLVMGPVFPYGRAWSIEDRSKLGDPKAGMSPPGFISGEGVLVIELCOL 324
Db 250 WDNKGAFAEKLIUVFPYGHNFILSNFTGIGAPTSAGAPGAPYAKESGIWAYEYIC-T 308
QY 325 FQKEWHIQDYENYAPGYNDKIWGYDDLASISCKLAFKLKELGVSVMVMSLENDDEFK 384
Db 309 FLKNGATQGWDAQEVYAYQGNVWVYDNIKSFIDIKAOGLKFNKFGGAMVMAIDLDLDDFT 368
QY 385 G-HCGP-KNPLLNKVNHNMGDEKNSPECILGPGSTTTPTTTPTTTPTTTPTTTPS 437
Db 369 GTFNCGKFFLI-----STLKKALGLQSASCTAPAOPIEPIITAAPSGS 411

Search completed: March 22, 2004, 07:45:51
Job time : 115.53 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 22, 2004, 06:42:54 ; Search time 44.7332 Seconds
(without alignments)
640.518 Million cell updates/sec

Title: US-09-662-293-15

Perfect score: 3107
Sequence: 1 MKTIVAILSMACIGLNMNAS.....IMCPPTGTTWCOEKLTCIGE 555

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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2: /cgn2_6/prodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/prodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/prodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/prodata/2/iaa/6C_COMB.pep:*
6: /cgn2_6/prodata/2/iaa/6D_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3107	100.0	555	US-09-292-225-15	Sequence 15, Appl
2	3107	100.0	555	US-09-292-225-18	Sequence 18, Appl
3	3014	97.0	536	US-09-292-225-21	Sequence 21, Appl
4	2542	81.8	509	US-09-292-225-35	Sequence 35, Appl
5	2542	81.8	509	US-09-292-225-38	Sequence 38, Appl
6	2475	79.7	490	US-09-292-225-41	Sequence 41, Appl
7	838.5	27.0	554	US-08-524-051-2	Sequence 2, Appl
8	838.5	27.0	554	US-09-052-778-16	Sequence 16, Appl
9	815.5	26.2	583	US-09-545-814-2	Sequence 2, Appl
10	815.5	26.2	583	US-09-545-814-5	Sequence 5, Appl
11	812.5	26.2	635	US-09-545-814-32	Sequence 32, Appl
12	811.5	26.1	559	US-09-545-814-14	Sequence 14, Appl
13	738	23.8	466	US-08-486-839-4	Sequence 4, Appl
14	738	23.8	466	US-09-151-011-4	Sequence 4, Appl
15	738	23.8	466	US-09-039-198A-2	Sequence 2, Appl
16	738	23.8	466	US-09-343-623-4	Sequence 4, Appl
17	738	23.8	466	US-08-877-599-2	Sequence 2, Appl
18	738	23.8	466	US-09-267-574-2	Sequence 2, Appl
19	732.5	23.6	387	US-08-486-839-6	Sequence 6, Appl
20	732.5	23.6	387	US-09-151-011-6	Sequence 6, Appl
21	732.5	23.6	387	US-09-039-198A-4	Sequence 4, Appl
22	732	23.6	466	US-09-343-623-6	Sequence 6, Appl
23	732	23.6	466	US-08-877-599-4	Sequence 4, Appl
24	732	23.6	466	US-09-267-574-4	Sequence 4, Appl
25	721.5	23.2	373	US-09-039-198A-14	Sequence 14, Appl
26	721.5	23.2	373	US-09-039-198A-15	Sequence 15, Appl
27	721.5	23.2	373	US-08-877-599-14	Sequence 14, Appl

28	721.5	23.2	373	4	US-08-877-599-15	Sequence 15, Appl
29	721.5	23.2	373	4	US-09-267-574-14	Sequence 14, Appl
30	721.5	23.2	373	4	US-09-267-574-15	Sequence 15, Appl
31	672.5	21.6	489	4	US-09-545-814-29	Sequence 29, Appl
32	650	20.9	383	4	US-09-459-748D-17	Sequence 17, Appl
33	630	20.3	385	2	US-08-694-915-2	Sequence 2, Appl
34	630	20.3	416	2	US-08-694-915-4	Sequence 4, Appl
35	630	20.3	423	4	US-08-850-348A-2	Sequence 2, Appl
36	420	13.5	442	3	US-09-052-778-2	Sequence 2, Appl
37	419.5	13.5	700	4	US-09-408-647A-2	Sequence 2, Appl
38	417	13.4	440	3	US-09-052-778-13	Sequence 13, Appl
39	412	13.3	423	1	US-07-939-501A-10	Sequence 10, Appl
40	412	13.3	423	1	US-07-939-501A-12	Sequence 12, Appl
41	411	13.2	389	1	US-07-939-501A-1	Sequence 1, Appl
42	411	13.2	389	3	US-08-448-398-7	Sequence 7, Appl
43	403.5	13.0	561	1	US-08-358-901-2	Sequence 2, Appl
44	403.5	13.0	561	1	US-08-566-347-2	Sequence 2, Appl
45	403.5	13.0	561	1	US-08-693-835-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-09-292-225-15
; Sequence 15, Application US/09292225
; Patent No. 6455866
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/09/292,225
; CURRENT FILING DATE: 1999-04-15
; EARLIER APPLICATION NUMBER: 60/098,909
; EARLIER FILING DATE: 1998-09-02
; EARLIER APPLICATION NUMBER: 60/085,295
; EARLIER FILING DATE: 1998-05-13
; EARLIER APPLICATION NUMBER: 60/098,565
; EARLIER FILING DATE: 1998-04-17
; EARLIER APPLICATION NUMBER: 09/062,013
; EARLIER FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 555
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-09-292-225-15

Query Match	100.0%;	Score 3107;	DB 4;	Length 555;
Best Local Similarity	100.0%;	Pred. No. 6.5e-241;		
Matches 555;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MKTIVAILSMACIGLNMNASIKRDNDYCNPMRIVCVGTWVSYYHKVDVPTTIEDIDPFK	60	
Db	1	MKTIVAILSMACIGLNMNASIKRDNDYCNPMRIVCVGTWVSYYHKVDVPTTIEDIDPFK	60	
Qy	61	CTHLMYGFAXIDEXKYTIQVDFPYQDDNHNHNSWEKRGYERFNNLRKNPELTMTISLGGWY	120	
Db	61	CTHLMYGFAXIDEXKYTIQVDFPYQDDNHNHNSWEKRGYERFNNLRKNPELTMTISLGGWY	120	
Qy	121	EGSKYSDMAANPTYRQOFTQSVLDFLOEYKFGDLDDWYPSGRLGNPKIDKQNYALV	180	
Db	121	EGSKYSDMAANPTYRQOFTQSVLDFLOEYKFGDLDDWYPSGRLGNPKIDKQNYALV	180	
Qy	181	RELKDAPEPHGYLLTAASVSGKIDRAYDIKEINKLFDWMNTYTDYHGGWENFYGHNA	240	
Db	181	RELKDAPEPHGYLLTAASVSGKIDRAYDIKEINKLFDWMNTYTDYHGGWENFYGHNA	240	
Qy	241	PLYKRPTDELHTYFNVNVTMTYLLNNGATRDKLVMGVFPFYGRAWSIEDRSKLKLGDA	300	

Db 241 PLYKRPDDELHTYFNNTWYVYLNNGATRDKLVGVVPYGRWSIEDRSKLGDP 300
Qy 301 KMSPPGPGISGEGVLSYIELCQFQKEWHIQYDEYNAPYGVNDKIWGYDDLASISC 360
Db 301 KMSPPGPGISGEGVLSYIELCQFQKEWHIQYDEYNAPYGVNDKIWGYDDLASISC 360
Qy 361 KLAFLKELGVSGVMVWSLENDDFKGHCQPKNPLLNKVNHNMGDEKNSFECILGPSTTTP 420
Db 361 KLAFLKELGVSGVMVWSLENDDFKGHCQPKNPLLNKVNHNMGDEKNSFECILGPSTTTP 420
Qy 421 TPPTTPT 480
Db 421 TPPTTPT 480
Qy 481 TSPPTTTEHTSETPKYTYVDGHLIKYKCEGDIPHPTNIHKYLVCVFVNGWVHIMPCP 540
Db 481 TSPPTTTEHTSETPKYTYVDGHLIKYKCEGDIPHPTNIHKYLVCVFVNGWVHIMPCP 540
Qy 541 PGTIWCQEKLTICGE 555
Db 541 PGTIWCQEKLTICGE 555

RESULT 2

US-09-292-225-18
; Sequence 18, Application US/09292225
; Patent No. 6455686
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/09/292,225
; CURRENT FILING DATE: 1999-04-15
; EARLIER APPLICATION NUMBER: 60/098,909
; EARLIER FILING DATE: 1998-09-02
; EARLIER APPLICATION NUMBER: 60/085,295
; EARLIER FILING DATE: 1998-05-13
; EARLIER APPLICATION NUMBER: 60/098,565
; EARLIER FILING DATE: 1998-04-17
; EARLIER APPLICATION NUMBER: 09/062,013
; EARLIER FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 18
; LENGTH: 555
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-09-292-225-18

Query Match 100.0%; Score 3107; DB 4; Length 555;
Best Local Similarity 100.0%; Pred. No. 6.5e-241;
Matches 555; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MXTYVAILSIMACIGLNMASIKRDHNDYSKNPMRIVCVGTWVYHKVDYPTTIEDIDPFK 60
Db 1 MXTYVAILSIMACIGLNMASIKRDHNDYSKNPMRIVCVGTWVYHKVDYPTTIEDIDPFK 60
Qy 61 CTHLMYGFADIDEYKTIQVDPYODDNHNSWEKRGYERFNNLKNPELTMTISLGGWY 120
Db 61 CTHLMYGFADIDEYKTIQVDPYODDNHNSWEKRGYERFNNLKNPELTMTISLGGWY 120
Qy 121 EGSEKYSMAANPTYROQFIQSVLDFQYKFDGLDLDWEYPSGLNPKDKONYLALV 180
Db 121 EGSEKYSMAANPTYROQFIQSVLDFQYKFDGLDLDWEYPSGLNPKDKONYLALV 180
Qy 181 RELKDAPEPHGYLLTAAVSPGKDKIDRAYDIIKELNKLFDWNNVMTYDHGGWENFYGHNA 240
Db 181 RELKDAPEPHGYLLTAAVSPGKDKIDRAYDIIKELNKLFDWNNVMTYDHGGWENFYGHNA 240

Qy 241 PLYKRPDDELHTYFNNTWYVYLNNGATRDKLVGVVPYGRWSIEDRSKLGDP 300
Db 241 PLYKRPDDELHTYFNNTWYVYLNNGATRDKLVGVVPYGRWSIEDRSKLGDP 300
Qy 301 KMSPPGPGISGEGVLSYIELCQFQKEWHIQYDEYNAPYGVNDKIWGYDDLASISC 360
Db 301 KMSPPGPGISGEGVLSYIELCQFQKEWHIQYDEYNAPYGVNDKIWGYDDLASISC 360
Qy 361 KLAFLKELGVSGVMVWSLENDDFKGHCQPKNPLLNKVNHNMGDEKNSFECILGPSTTTP 420
Db 361 KLAFLKELGVSGVMVWSLENDDFKGHCQPKNPLLNKVNHNMGDEKNSFECILGPSTTTP 420
Qy 421 TPPTTPT 480
Db 421 TPPTTPT 480
Qy 481 TSPPTTTEHTSETPKYTYVDGHLIKYKCEGDIPHPTNIHKYLVCVFVNGWVHIMPCP 540
Db 481 TSPPTTTEHTSETPKYTYVDGHLIKYKCEGDIPHPTNIHKYLVCVFVNGWVHIMPCP 540
Qy 541 PGTIWCQEKLTICGE 555
Db 541 PGTIWCQEKLTICGE 555

RESULT 3

US-09-292-225-21
; Sequence 21, Application US/09292225
; Patent No. 6455686
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/09/292,225
; CURRENT FILING DATE: 1999-04-15
; EARLIER APPLICATION NUMBER: 60/098,909
; EARLIER FILING DATE: 1998-09-02
; EARLIER APPLICATION NUMBER: 60/085,295
; EARLIER FILING DATE: 1998-05-13
; EARLIER APPLICATION NUMBER: 60/098,565
; EARLIER FILING DATE: 1998-04-17
; EARLIER APPLICATION NUMBER: 09/062,013
; EARLIER FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 21
; LENGTH: 536
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-09-292-225-21

Query Match 97.0%; Score 3014; DB 4; Length 536;
Best Local Similarity 100.0%; Pred. No. 1.8e-233;
Matches 536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 20 SIKRDHNDYSKNPMRIVCVGTWVYHKVDYPTTIEDIDPFKCTHLMYGFADIDEYKTIQ 79
Db 1 SIKRDHNDYSKNPMRIVCVGTWVYHKVDYPTTIEDIDPFKCTHLMYGFADIDEYKTIQ 60
Qy 80 VFDPYODDNHNSWEKRGYERFNNLKNPELTMTISLGGWYEGSEKYSMAANPTYROQF 139
Db 61 VFDPYODDNHNSWEKRGYERFNNLKNPELTMTISLGGWYEGSEKYSMAANPTYROQF 120
Qy 140 IQSVLDFQYKFDGLDLDWEYPSGLNPKDKONYLALVRELKDAPEPHGYLLTAAVS 199
Db 121 IQSVLDFQYKFDGLDLDWEYPSGLNPKDKONYLALVRELKDAPEPHGYLLTAAVS 180
Qy 200 PGKDKIDRAYDIIKELNKLFDWNNVMTYDHGGWENFYGHNAPLYKRPDDELHTYFN 259
Db 181 PGKDKIDRAYDIIKELNKLFDWNNVMTYDHGGWENFYGHNAPLYKRPDDELHTYFN 240

Qy	260	YTHYYLNNGATRD	KLVMGPYPY	GRAWSIEDRS	KLGDPAKGMSP	PGFISGEGVLSYI	319
Db	241	YTHYYLNNGATRD	KLVMGPYPY	GRAWSIEDRS	KLGDPAKGMSP	PGFISGEGVLSYI	300
Qy	320	ELCOLQKBEWHIQY	DEYYNA	PVGYNDK	IWGYDDLASISCKLAFLKEL	GVGMVWSLE	379
Db	301	ELCOLQKBEWHIQY	DEYYNA	PVGYNDK	IWGYDDLASISCKLAFLKEL	GVGMVWSLE	360
Qy	380	NDPFKGHCQPKPLN	KNVNMINGDEKNS	FECILGPS	TTTPTTTPTTTPTTTPTT	PTTPTT	439
Db	361	NDPFKGHCQPKPLN	KNVNMINGDEKNS	FECILGPS	TTTPTTTPTTTPTTTPTT	PTTPTT	420
Qy	440	TPTTTSPPTTTPTT	SPPTTPTTPTT	PTTPTTPTT	PTTPTTPTT	PTTPTT	499
Db	421	TPTTTSPPTTTPTT	SPPTTPTTPTT	PTTPTTPTT	PTTPTTPTT	PTTPTT	480
Qy	500	VDGHLKCKYKEGDI	PHPTNIHKYL	VFCEVNGGWWH	IMPCDPGT	IWQCKLTIGE	555
Db	481	VDGHLKCKYKEGDI	PHPTNIHKYL	VFCEVNGGWWH	IMPCDPGT	IWQCKLTIGE	536

RESULT 4
 US-09-292-225-35
 ; Sequence 35, Application US/09292225
 ; Patent No. 6455686
 ; GENERAL INFORMATION:
 ; APPLICANT: McCall, Catherine A.
 ; APPLICANT: Hunter, Shirley Wu
 ; APPLICANT: Weber, Eric R.
 ; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
 ; TITLE OF INVENTION: AND USES THEREOF
 ; FILE REFERENCE: AU-2-C3
 ; CURRENT APPLICATION NUMBER: US/09/292,225
 ; CURRENT FILING DATE: 1999-04-15
 ; EARLIER APPLICATION NUMBER: 60/098,909
 ; EARLIER FILING DATE: 1998-09-02
 ; EARLIER APPLICATION NUMBER: 60/085,295
 ; EARLIER FILING DATE: 1998-05-13
 ; EARLIER APPLICATION NUMBER: 60/098,565
 ; EARLIER FILING DATE: 1998-04-17
 ; EARLIER APPLICATION NUMBER: 09/062,013
 ; EARLIER FILING DATE: 1998-04-17
 ; NUMBER OF SEQ ID NOS: 49
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 35
 ; LENGTH: 509
 ; TYPE: PRT
 ; ORGANISM: Dermatophagoides farinae
 US-09-292-225-35

Db	241	PLYKRPDETDLHTTYPNVNYTHYYLNNAGTRDKLVNMGVPPFYGRAMSIEDRSKVLGDPA	300
Qy	301	KGMSPPGFTISBEGVLSYIELCOLFOKEEWHIQVDEYINAPYGNDKIWNVYDDLASISC	360
Db	301	KGMSPPGFTISBEGVLSYIELCOLFOKEEWHIQVDEYINAPYGNDKIWNVYDDLASISC	360
Qy	361	KLAFKLKELGVSGVMVWSLENDDPKGHCGPKNPLLNKVNHNINGDEKNSPECILGPSTTTP	420
Db	361	KLAFKLKELGVSGVMVWSLENDDPKGHCGPKNPLLNKVNHNINGDEKNSPECILGPSTTTP	420
Qy	421	TPPT	480
Db	421	TPPT	434
Qy	481	TPSPPTTHTSTPKYTYTVDSGHLIKCYKCEGDIPHPTNIHKYLVCRFV--NGSGWVHIM	537
Db	435	---PTTDTSTSPKTYTYTVDSGHLIKCYKQYLPHPDIVEKYLVCETIATPNGSGWVHIM	491
Qy	538	PCPPPGTINCQEKLTJCIGE	555
Db	492	DCPKGTRWHTATLKNCIOE	509

RESULT 5
US-09-292-225-38
; Sequence 38, Application US/09292225
; Patent No. 6455686
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/09/292,225
; CURRENT FILING DATE: 1999-04-15
; EARLIER APPLICATION NUMBER: 60/098,909
; EARLIER FILING DATE: 1998-09-02
; EARLIER APPLICATION NUMBER: 60/085,295
; EARLIER FILING DATE: 1998-05-13
; EARLIER APPLICATION NUMBER: 60/098,565
; EARLIER FILING DATE: 1998-04-17
; EARLIER APPLICATION NUMBER: 09/062,013
; EARLIER FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 38
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-09-292-225-38

	Local Similarity	81.7%;	Pred. No. 1.1e-195;	Mismatches	24;	Indels	52;	Gaps	2
Qy	1	MKTIYAILSIMACIGLMMNASIKRDNHNSKNPMRIVCVGVTWSVYHKVDPTTIEDIDPFK	60	:	:	:	:	:	:
Db	1	MKTTTFALFCIWACIGLMMNAATKRDNHNSKNPMRIVCVGVTWSVYHKVDPTTIEDIDPFK	60	:	:	:	:	:	:
Qy	61	CTHLMYGEAKIDYKTTIOVFOPYODDNHNSWEKRGYERFNLLKRPPELLTMTTISLGGWY	120	:	:	:	:	:	:
Db	61	CTHLMYGFPAKIDYKTTIOVFOPYODDNHNSWEKRGYERFNLLKRPPELLTMTTISLGGWY	120	:	:	:	:	:	:
Qy	121	EGSEKYSDMAANPTYRQQPIQSVLDFLOEYKFDGLDLDWEYPGSRLGNPKIDKQNTIALIV	180	:	:	:	:	:	:
Db	121	EGSEKYSDMAANPTYRQQFVQSVLDFLOEYKFDGLDLDWEYPGSRLGNPKIKQNTIIV	180	:	:	:	:	:	:
Qy	181	REUKDAFEHGYLLTAASVPGKDKIDRAVDIKELNKLPEDMNMVMTYDYGGSNPFVGHNA	240	:	:	:	:	:	:
Db	181	REUKDAFEHGYLLTAASVPGKDKIDVAIEUKELNQLDMMNMVMTYDYGGSNPFVGHNA	240	:	:	:	:	:	:
Qy	241	PLYKRPDETDLHTYFNNVNTWHTYIYLNAGTRDKLVMGVPPYGRAWIEDRSKLKLGDA	300	:	:	:	:	:	:

Query Match	81.8%;	Score 2542;	DB 4;	Length 509;
Best Local Similarity	81.7%;	Pred. No. 1.1e-195;		
Matches 456;	Conservative 24;	Mismatches 26;	Indels 52;	Gaps 2
Qy	1	MKTIVAISIMACIGLMNASIKRDNHYSKNPRLVCYVGTWSVYHKVDPTYTIEDIDPFK	60	
Db	1	MKTIPALFCIWACIGLMNAATKRDHNYSKNPRLVCYVGTWSVYHKVDPTYTIEDIDPFK	60	
Qy	61	CTHLMYGFAKIDYEKYTTQVDPDPQDDNHNSWEKRGYERFNNRLKNPELTWMSLGGY	120	
Db	61	CTHLMYGFAKIDYEKYTTQVDPDPQDDNHNSWEKRGYERFNNRLKNPELTWMSLGGY	120	
Qy	121	EGSEKYSDMAANPTTRQOFIGSLVDFLOEYKFDGLDLDWEYPGSLGNPKIKDKQNYLALV	180	
Db	121	EGSEKYSDMAANPTTRQOFVQSLVDFLOEYKFDGLDLDWEYPGSLGNPKIKDKQNYLTV	180	
Qy	181	RELKDAFEHPGVILLTAAVSPGKKIDRAYDIKELNKLPDWMNVTYDYGCGWENFVGHNA	240	
Db	181	RELKEAFEPGVILLTAAVSPGKKIDVAYELKELNQLDFWMNVTYDYGCGWENFVGHNA	240	
Qy	241	PLYKRPDEPDELHTYTFNNYTHWYLLNNGATPRDKLVGMGVFYGRAWSIDRSKCLKLGDPA	300	

[illegible]

```

RESULT 6
US-09-292-225-41
; Sequence 41, Application US/09292225
; Patent No. 6455686
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/09/292,225
; CURRENT FILING DATE: 1999-04-15
; EARLIER APPLICATION NUMBER: 60/098,909
; EARLIER FILING DATE: 1998-09-02
; EARLIER APPLICATION NUMBER: 60/085,295
; EARLIER FILING DATE: 1998-05-13
; EARLIER APPLICATION NUMBER: 60/098,565
; EARLIER FILING DATE: 1998-04-17
; EARLIER APPLICATION NUMBER: 09/062,013
; EARLIER FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 41
; LENGTH: 490
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-09-292-225-41

```

Query Match	79.7%	Score 2475;	DB 4;	Length 490;
Best Local Similarity	82.5%;	Pred. No. 2.5e-190;		
Matches 443;	Conservative 21;	Mismatches 21;	Indels 52;	Gaps 2;
QY	22	KRDHNDYSEKNP	RVYCVYGVTSVTHKVD	PTTIEDIDPFKCTHLMYGAFKIDSEYKTIQVF 81
DB	3	KRDHNNYSEKNP	RVYCVYGVTSVTHKVD	PTTIEDIDPFKCTHLMYGAFKIDSEYKTIQVF 62
QY	82	DYQDDNNHSEK	NGYERFNNLR	LKNPELTMTISLGGWYEGSEKYSMDMAANPTTYRQQFTQ 141
DB	63	DPFQDDNNHSE	KHGYERFNNLR	LKNPELTMTISLGGWYEGSEKYSMDMAANPTTYRQQFVQ 122
QY	142	SVLDFLQYKFDG	LDDLWYEGPSRLGNPK	IKDKNYLALVRELKDAPEFHGYLLTAAVSPG 201
DB	123	SVLDFLQYKFDG	LDDLWYEGSSRLGNPK	IKDKNYLTLVRELKEAPEFGYLLTAAVSPG 182
QY	202	KDKIDRAVDIK	ELKNKLFDMNNVM	TYDHHGWNFPYGHNAPLYKRPDETDELTYTFNNVNT 261
DB	183	KDKIDVAYELK	ELKNLQFDMNNVM	TYDHHGWNVFNHNAPLYKRPDETDELTYTFNNVNT 242

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262 QY 262 MHYYLNGATRDKLVNGVPPFYGRAMSIEDRSKVLGDPKAGMSPPGFITGEGVLSYIEL 321
243 Db 243 MHYYLNGATRDKLVNGVPPFYGRAMSIEDRSKVLGDPKAGMSPPGFITGEGVLSYIEL 302
QY 322 CQLFQKEWHIQYDEVYNAPYGVNDKIWGYDDLASISCKLAFKELGUGVGMVWSLEND 381
Db 303 CQLFQKEWHIQYDEVYNAPYGVNDKIWGYDDLASISCKLAFKELGUGVGMVWSLEND 362
QY 382 DFKGHGCGPNPLLNKVVHNMINGDEKNSFFCILGPSITTTPTTPTTPTTPTTPTTPTTTP 441
Db 363 DFKGHGCGPNPLLNKVVHNMINGDEKNSYECLLGPSITTTPTTPTTPTTPTTPTTPTT 415
QY 442 TTTPTSTTTTPTTPTPTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTT 501
Db 416 -----PTTDTSTSETPKYTYID 433
QY 502 GHLIKYKGBDHPHTNIHKYLCEFV---NGGWWVHIMCPPGTTWCQEKLCIG 555
Db 434 GHLIKYKGYLPHPTDVHKLVCYFIATPNGGWWVHIMDCPKGTRWHTLKNCIQ 490

RESULT 7
US-08-524-051-2
; Sequence 2, Application US/08524051
; Patent No. 5866788
; GENERAL INFORMATION:
; APPLICANT: Kramer, Karl J.
; APPLICANT: Muthukrishnan, Subbaratnam
; APPLICANT: Choi, Hee Kyung
; APPLICANT: Corpuz, Iolita
; APPLICANT: Gopalakrishnan, Bhuvana
; TITLE OF INVENTION: RECOMBINANT CHITINASE AND USE THEREOF AS
; TITLE OF INVENTION: A BIODE
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hovey, Williams, Timmons & Collins
; STREET: 2405 Grand Blvd., Suite 400
; CITY: Kansas City
; STATE: MO
; COUNTRY: USA
; ZIP: 64108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/524,051
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Collins, John M.
; REGISTRATION NUMBER: 26,262
; REFERENCE/DOCKET NUMBER: 22875-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (816)474-9050
; TELEFAX: (816)474-9057
; TELEX: 434-363
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 554 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-524-051-2

```

Query Match	27.0%;	Score 838.5;	DB 2;	Length 554;
Best Local Similarity	35.4%;	Pred. NO. 4.9e-59;		
Matches 208;	Conservative	79;	Mismatches 210;	Indels 91; Gaps 20;
QY	6	AILSINACIGLNNASIKRDHNDYSKNPMRIVCVGTWGVYHK-	VDPTTIEDIDPFKCTHL	64
Db	3	ATLATLAVLATATV-----QSDSRATVCFVSNWAVRPGVGVGIEDIEVEKCTHI		55

QY 65 MYGFAKIDYKYTIQVDFPDYDDNHNHNSWEKRGYERFNNLRKLNPELTJTWISLGGWYEGSE 124
DB 56 IYISFIGVTGENSEVLIDPELD-----VDKNGFRNTSLRSHPSVKFWVAVGGWABGS 110
QY 125 KYSDMAANPTYROOFTQSVLDLFIQYKFDGLDLDWEYPGSR-LGNPKIDKONYLALVREL 183
DB 111 KYSHWAKSTRMSFIRSVSLKYYDFDGLDLDWEYPGAADRGGSFSDKDFLYLVQEL 170
QY 184 KDAP--EPHGYSLLTAAPSGPKIDRAYDIKELNKLFDMMNMTYDYHGGWENFYGHAP 241
DB 171 RRAFIRVGKWELTAAVPLANFLRMHGVHVPCLQELDAIHVMSYDLRGNWAGFADVHSP 230
QY 242 LYKRPDETDELHTYFNVNYTHYYLNGATRDKLVMGVPPFYGPAWSIED-----290
DB 231 LYKRPD--QWYKELVNDGLHWEKGCPSNKLTVGIPFYGRSFTLSAGNNYGLGTPI 289
QY 291 RSKLGLGDPKAGMSPPGFISGREGVLSYIELCOLFOKEE--WHIOYDEYNNAPYGYNDKI 348
DB 290 NKEAGGDPAPYTNATG-----WAYYEICTEVDKDDSGTWKWDGCKPCPYAYKGTQ 342
QY 349 WGYDDLASISCKLAFELKELGVSGVMVWSLENDDFKGCPCPNLKNVNMINGDEKNS 408
DB 343 WGYEDPRSVEIKNNWIKQKGYLGAMTWAIDMDDFQGLCGEKNPLIKILHKMS-----396
QY 409 FECILGPSTTTPTTPTTPT-----TPTTPPS-----PTTPTTSPSTPTTTPSP 456
DB 397 -----SYTVPPPHENTTPTPEWARPPSTPSDPSGDPPTPTTTAKPASTTKTKTKT 449
QY 457 TPTTTPSPIT-----PTP-TTPTPAPTSTPSPTTHTSETPKYTYTVDGHLI 505
DB 450 TTTAKPQSVIDEENDINVRPEKPEPEVEVP-PTENE-----VDGSEI 497
QY 506 KCKYEGD-IPHTNIHKYLVCDFVNGVWVHIMPCPPGIWCOEKLTC 552
DB 498 -CNSDDQYIPDKKXCHDKYWC--VNGE--AMQFSCQHGTVFVVELNVC 540

RESULT 8
US-09-552-778-16
; Sequence 16, Application US/09052778A
; Patent No. 6060590
; GENERAL INFORMATION:
; APPLICANT: Bryant, Peter J.
; APPLICANT: Kawamura, Kazuo
; TITLE OF INVENTION: CHITINASE RELATED PROTEINS AND METHODS
; FILE OF INVENTION: OF USE
; FILE REFERENCE: 07306/015001
; CURRENT APPLICATION NUMBER: US/09/052,778A
; PRIOR FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 554
; TYPE: PRT
; ORGANISM: Manduca sexta
US-09-552-778-16

Query Match 27.0%; Score 838.5; DB 3; Length 554;
Best Local Similarity 35.4%; Pred. No. 4.8e-59;
Matches 208; Conservative 79; Mismatches 210; Indels 91; Gaps 20;
QY 6 AIIISWACIGLMAASIKEDNDYKNNPMRIVCVGTWVTHK-VDPYTIETDIPFKCTHL 64
DB 3 ATLATLAVLATAV-----QSDSRARIVCVFNSWVYRPGVGRYGIEDIPVEKCTHI 55
QY 65 MYGFAKIDYKYTIQVDFPDYDDNHNHNSWEKRGYERFNNLRKLNPELTJTWISLGGWYEGSE 124
DB 56 IYISFIGVTGENSEVLIDPELD-----VDKNGFRNTSLRSHPSVKFWVAVGGWABGS 110
QY 125 KYSDMAANPTYROOFTQSVLDLFIQYKFDGLDLDWEYPGSR-LGNPKIDKONYLALVREL 183
DB 111 KYSHWAKSTRMSFIRSVSLKYYDFDGLDLDWEYPGAADRGGSFSDKDFLYLVQEL 170

QY 184 KDAP--EPHGYSLLTAAPSGPKIDRAYDIKELNKLFDMMNMTYDYHGGWENFYGHAP 241
DB 171 RRAFIRVGKWELTAAVPLANFLRMHGVHVPCLQELDAIHVMSYDLRGNWAGFADVHSP 230
QY 242 LYKRPDETDELHTYFNVNYTHYYLNGATRDKLVMGVPPFYGPAWSIED-----290
DB 231 LYKRPD--QWYKELVNDGLHWEKGCPSNKLTVGIPFYGRSFTLSAGNNYGLGTPI 289
QY 291 RSKLGLGDPKAGMSPPGFISGREGVLSYIELCOLFOKEE--WHIOYDEYNNAPYGYNDKI 348
DB 290 NKEAGGDPAPYTNATG-----WAYYEICTEVDKDDSGTWKWDGCKPCPYAYKGTQ 342
QY 349 WGYDDLASISCKLAFELKELGVSGVMVWSLENDDFKGCPCPNLKNVNMINGDEKNS 408
DB 343 WGYEDPRSVEIKNNWIKQKGYLGAMTWAIDMDDFQGLCGEKNPLIKILHKMS-----396
QY 409 FECILGPSTTTPTTPTTPT-----TPTTPPS-----PTTPTTSPSTPTTTPSP 456
DB 397 -----SYTVPPPHENTTPTPEWARPPSTPSDPSGDPPTPTTTAKPASTTKTKTKT 449
QY 457 TPTTTPSPIT-----PTP-TTPTPAPTSTPSPTTHTSETPKYTYTVDGHLI 505
DB 450 TTTAKPQSVIDEENDINVRPEKPEPEVEVP-PTENE-----VDGSEI 497
QY 506 KCKYEGD-IPHTNIHKYLVCDFVNGVWVHIMPCPPGIWCOEKLTC 552
DB 498 -CNSDDQYIPDKKXCHDKYWC--VNGE--AMQFSCQHGTVFVVELNVC 540

RESULT 9
US-09-545-814-2
; Sequence 2, Application US/09545814
; Patent No. 6416977
; GENERAL INFORMATION:
; APPLICANT: Becher, Anna M.
; TITLE OF INVENTION: FLEA CHITINASE NUCLEIC ACID MOLECULES, PROTEINS AND
; FILE OF INVENTION: USES THEREOF
; FILE REFERENCE: FC-5-C1
; CURRENT APPLICATION NUMBER: US/09/545,814
; CURRENT FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/128,833
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 583
; TYPE: PRT
; ORGANISM: Ctenocephalides felis
US-09-545-814-2

Query Match 26.2%; Score 815.5; DB 4; Length 583;
Best Local Similarity 34.6%; Pred. No. 3.6e-57;
Matches 198; Conservative 94; Mismatches 205; Indels 75; Gaps 23;
QY 7 ILSIMACIGLMAASIKEDNDYKNNPMRIVCVGTWVTHK-VDPYTIETDIPFKCTHL 65
DB 6 LLAVLCALAISSINTV-----EASQKARIVCFNSWVYRPGVGRYGIEDIPVLCITIV 61
QY 66 YGFAKIDYKYTIQVDFPDYDDNHNHNSWEKRGYERFNNLRKLNPELTJTWISLGGWYEGSE 125
DB 62 YSFIGVDDKDSVLVIDPELDIDN-----GPKNFTNLKTHFNVLKQIAGVGGWABGSK 116
QY 126 YSDMAANPTYROOFTQSVLDLFIQYKFDGLDLDWEYPGSR-LGNPKIDKONYLALVREL 184
DB 117 YSTVAERKRSAPFIRSVDFMVEYKFDGDFLDWEYPGAADRGGSFSDKDFLYLVQEL 176
QY 185 DAFEPHG--YLLTAAPSGPKIDRAYDIKELNKLFDMMNMTYDYHGGWENFYGHAP 242
DB 177 RAFNKGQKWEITWAVPIAKFRLQEGVHVPCLQELDAIHVMSYDLRGNWAGFADTHSP 236
QY 243 YKRPDETDELHTYFNVNYTHYYLNGATRDKLVMGVPPFYGPAWSIEDRSK-LKLG--D 298

Db 237 YRRPHD-QYAYEKLNVNDGLQLWDMGCPANKLVGVFPYGRSFTLSNKNDRYLGTYIN 295
QY 299 PAKGWSPPGFTSGEEGLSYTELQQLFQ--KEEWHIQYDEYNAPYGYNDKIWGVYDDL 356
Db 296 KEAGGEPGFTYNATGFTSYEIECLEVDPSKGTWKDDEHGKVPYAYKQNGWGYEDPK 355
QY 357 SISCKLAPLKLGLVSGVMVWSLENDDFKHCG-PKNPLLNKVNHNMGDEKNSFECILGP 415
Db 356 SVALKMEFIKSGYGGAMTWMDDDFQVCSDDKHTLAVIMHDY----KNYIVPEFDS 411
QY 416 STTTPTP--TTTPTPTPTPTPTPTPT--TPSPT--TPPTPTPTPTPTPTPTPTPTPT 471
Db 412 SRITRPEWAKPPTSPQEP--DDTPYIPTTHAPKSRKTRKPKPT--TTTAAATTPVAT 468
QY 472 TPTAPTSTSPPTTE-----HTSETP-----KYTTYVDGHLIKCYKEGDIPIPT 517
Db 469 -----TTTEHHHHHEEKSEQDNQVGSQDTTATD---VDCSQEDYLPH-E 511
QY 518 NIHKLVCFFVNGGMMVH-----IMPCPPGTIW 545
Db 512 DCKNYRC-----VHGEAVLFTCREGTVY 535
RESULT 10
US-09-545-814-5
; Sequence 5, Application US/09545814
; Patent No. 6416977
; GENERAL INFORMATION:
; APPLICANT: Becher, Anna M.
; TITLE OF INVENTION: FLEA CHITINASE NUCLEIC ACID MOLECULES, PROTEINS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: FC-5-C1
; CURRENT APPLICATION NUMBER: US/09/545,814
; CURRENT FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/128,833
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 5
; LENGTH: 583
; TYPE: PRT
; ORGANISM: Ctenocephalides felis
US-09-545-814-5
Query Match 26.2%; Score 815.5; DB 4; Length 583;
Best Local Similarity 34.6%; Pred. No. 3.6e-57;
Matches 198; Conservative 94; Mismatches 205; Indels 75; Gaps 23;
QY 7 ILSIWACIGLWNASIKRDNDYKSNPMRIVCYVGTWVSYHK-VDPYTIEDIDPFKCTHLM 65
Db 6 LLAVLCAIAISSINTV----EASDQKARIVCYFSNVAWYRPGIGRYGIEDIPVDLCTHIV 61
QY 66 YGFAKIDYKVTIQVDFPYQDDNHNSEKRGYERPNLRLKNPELTMTWISLGGWYEGSEK 125
Db 62 YSFIGVDDKWSVLVIDPELDIDN-----GFKNFTNLRKIHNVKLQIAGVGAEGGKK 116
QY 126 YSDMAANPTYRQOFTSQSLDFLOEYKFDGLDWEYPGSR-LGNPKIDKQNYLALVRELK 184
Db 117 YSTWVAEKRKSAFIRSVVDPMNEYKFDGLDWEYPGAADRGSGFSKDKFLYFVQELR 176
QY 185 DAFEPHG--YLLTAASPGKDKIDRAYDIKEINLKFDMNVMYTYDYGHWENFYGHNAFL 242
Db 177 RAFNKGQKNWEITWAVPTAKFRLQEGYHVPELCELLDAIHVMSYDLRGNWAGFADTHSPL 236
QY 243 YKRDETDLHTYFNVTMYHLYNNGATRKLVNGVDFPYGRAWSIEDRSK-LKLG---D 298
Db 237 YRRPHD-QYAYEKLNVNDGLQLWDMGCPANKLVGVFPYGRSFTLSNKNDRYLGTYIN 295
QY 299 PAKGWSPPGFTSGEEGLSYTELQQLFQ--KEEWHIQYDEYNAPYGYNDKIWGVYDDL 356
Db 296 KEAGGEPGFTYNATGFTSYEIECLEVDPSKGTWKDDEHGKVPYAYKQNGWGYEDPK 355
QY 357 SISCKLAPLKLGLVSGVMVWSLENDDFKHCG-PKNPLLNKVNHNMGDEKNSFECILGP 415

Db 356 SVALKMEFIKSGYGGAMTWMDDDFQVCSDDKHTLAVIMHDY----KNYIVPEFDS 411
QY 416 STTTPTP--TTTPTPTPTPTPTPTPT--TPSPT--TPPTPTPTPTPTPTPTPTPTPT 471
Db 412 SRITRPEWAKPPTSPQEP--DDTPYIPTTHAPKSRKTRKPKPT--TTTAAATTPVAT 468
QY 472 TPTAPTSTSPPTTE-----HTSETP-----KYTTYVDGHLIKCYKEGDIPIPT 517
Db 469 -----TTTEHHHHHEEKSEQDNQVGSQDTTATD---VDCSQEDYLPH-E 511
QY 518 NIHKLVCFFVNGGMMVH-----IMPCPPGTIW 545
Db 512 DCKNYRC-----VHGEAVLFTCREGTVY 535
RESULT 11
US-09-545-814-32
; Sequence 32, Application US/09545814
; Patent No. 6416977
; GENERAL INFORMATION:
; APPLICANT: Becher, Anna M.
; TITLE OF INVENTION: FLEA CHITINASE NUCLEIC ACID MOLECULES, PROTEINS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: FC-5-C1
; CURRENT APPLICATION NUMBER: US/09/545,814
; CURRENT FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/128,833
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 32
; LENGTH: 635
; TYPE: PRT
; ORGANISM: Tagged Ctenocephalides felis
US-09-545-814-32
Query Match 26.2%; Score 812.5; DB 4; Length 635;
Best Local Similarity 34.6%; Pred. No. 7e-57;
Matches 198; Conservative 93; Mismatches 206; Indels 75; Gaps 23;
QY 7 ILSIWACIGLWNASIKRDNDYKSNPMRIVCYVGTWVSYHK-VDPYTIEDIDPFKCTHLM 65
Db 7 LLAVLCAIAISSINTV----EASDQKARIVCYFSNVAWYRPGIGRYGIEDIPVDLCTHIV 62
QY 66 YGFAKIDYKVTIQVDFPYQDDNHNSEKRGYERPNLRLKNPELTMTWISLGGWYEGSEK 125
Db 63 YSFIGVDDKWSVLVIDPELDIDN-----GFKNFTNLRKIHNVKLQIAGVGAEGGKK 117
QY 126 YSDMAANPTYRQOFTSQSLDFLOEYKFDGLDWEYPGSR-LGNPKIDKQNYLALVRELK 184
Db 118 YSTWVAEKRKSAFIRSVVDPMNEYKFDGLDWEYPGAADRGSGFSKDKFLYFVQELR 177
QY 185 DAFEPHG--YLLTAASPGKDKIDRAYDIKEINLKFDMNVMYTYDYGHWENFYGHNAFL 242
Db 178 RAFNKGQKNWEITWAVPTAKFRLQEGYHVPELCELLDAIHVMSYDLRGNWAGFADTHSPL 237
QY 243 YKRDETDLHTYFNVTMYHLYNNGATRKLVNGVDFPYGRAWSIEDRSK-LKLG---D 298
Db 238 YRRPHD-QYAYEKLNVNDGLQLWDMGCPANKLVGVFPYGRFFTLSNKNDRYLGTYIN 296
QY 299 PAKGWSPPGFTSGEEGLSYTELQQLFQ--KEEWHIQYDEYNAPYGYNDKIWGVYDDL 356
Db 297 KEAGGEPGFTYNATGFTSYEIECLEVDPSKGTWKDDEHGKVPYAYKQNGWGYEDPK 356
QY 357 SISCKLAPLKLGLVSGVMVWSLENDDFKHCG-PKNPLLNKVNHNMGDEKNSFECILGP 415
Db 357 SVALKMEFIKSGYGGAMTWMDDDFQVCSDDKHTLAVIMHDY----KNYIVPEFDS 412
QY 416 STTTPTP--TTTPTPTPTPTPTPTPT--TPSPT--TPPTPTPTPTPTPTPTPTPTPT 471
Db 413 SRITRPEWAKPPTSPQEP--DDTPYIPTTHAPKSRKTRKPKPT--TTTAAATTPVAT 469

QY 472 TPTAPTSTRPTTTE-----HTSETP-----KYTTVDGHLIKYKKGDIHPT 517
Db 470 -----TTTEHHHHHEEKSEQDNQVSGDQTATD---VDCSEDYLPB-E 512
QY 518 NIHKLVCFFVNGGWWVH-----IMPCPPGTIW 545
Db 513 DCKKYRC-----VHGEAVLFTCRBGTVY 536

RESULT 12
US-09-545-814-14
; Sequence 14, Application US/09545814
; Patent No. 6416977
; APPLICANT: Becher, Anna M.
; TITLE OF INVENTION: FLEA CHITINASE NUCLEIC ACID MOLECULES, PROTEINS AND
; FILE REFERENCE: PC-5-C1
; CURRENT APPLICATION NUMBER: US/09/545,814
; CURRENT FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/128,833
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 14
; LENGTH: 559
; TYPE: PRT
; ORGANISM: Ctenocephalides felis
US-09-545-814-14

Query Match 26.1%; Score 811.5; DB 4; Length 559;
Best Local Similarity 35.8%; Pred. No. 7.1e-57;
Matches 195; Conservative 86; Mismatches 193; Indels 71; Gaps 22;

QY 34 RIVCYGVTSVTHK-VDPYTTIEDIDPFKCTHLMYGFADKIDYKTYIQVDPYQDDNHSW 92
Db 5 RIVCYFSNWAYRPGIRYGIEDIPVLCITHIVSFIGVDDKMSVLVIDPDLIDDN-- 62
QY 93 ERKGYERFNNLRKMPETLMTSLGWEYEGSEKYSMDAANTYRQFTQSVLDLFLQEVKF 152
Db 63 ---GFKFNLRKIHFNKQLAVGNAEGGKYSTVAEKRSASFIRSVDFMNEYKF 119
QY 153 DGLDLWDWEYVPSGR-LGNPKIDKQNTLALVRELKDAFEPHG--YLLTAAVSPGKKIDRAY 209
Db 120 DGFDLWDWEYVPGADRGGSFSDKXFLYFQELRRAFNKQGNWELTMAVPIAKFRLQEGY 179
QY 210 DTKELNKLFDWMNVMTYDYGWENFYGHNAFLYKRPDETDELHTYFNVTMTHYLLNG 269
Db 180 HVPCLCELLDAITHVMSYDLRGNWAGFADTHSPLYRRPHD-QVAYEKLNVNDGLQLWVDMG 238
QY 270 ATRDKLVGVPPYGRAWSIEDRSK-LKLG---DPAKGMSPGPGFSGEGLVSYIELCOLF 325
Db 239 CPANLVLVGVPPYGRSFTLSNSNDYRLGTINKEAGGEGPGPYTNATGFSYVEICLEV 298
QY 326 Q--KEEMHIQVDEYNAPYGVNDKLVGVYDGLASISCKLAFELKELGVGMVWLENDDF 383
Db 299 DDPKSGWTKMDHGHQKPYAYKGNQVGYEDPKSVALKQEFIKSGYGMATWIDMDDF 358
QY 384 KGHCG-PKNPLLNKVNMMINGDEKNSFECILGPSFTTPTP--TTPPTPTPTTPTSPPT 440
Db 359 QGVCSDDKXHTLAVIMHDYK---KNYIVPEPDSRITRPERWAKPPTSPQEP-DDTPIYI 413
QY 441 PTT-TPSPPT-PTTTPSPPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTT 493
Db 414 PTHAPKPSRPTKPKPT--TTTVAATTVPAT-----TTTEHHHHHEEEK 458
QY 494 P-----KYTTVDGHLIKYKKGDIHPTNIHKLVLCFVNGGWVH-----IMPCP 540
Db 459 PSEQDNQVSGDQTATD---VDCSEDYLPB-EDCNKYRC-----VHGEAVLFTCR 506
QY 541 PGTIW 545
Db 507 EGTIV 511

RESULT 13
US-08-486-839-4
; Sequence 4, Application US/08486839
; Patent No. 5928928
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: A human chitinase, its recombinant
; TITLE OF INVENTION: production, its use for decomposing chitin, its use
; TITLE OF INVENTION: in therapy or prophylaxis against infection diseases.
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann & Baron
; STREET: 350 Jericho Turnpike
; CITY: Jericho
; STATE: New York
; COUNTRY: United States of America
; ZIP: 11758
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,839
; FILING DATE: 07 - June - 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Baron, Ronald J.
; REGISTRATION NUMBER: 29,281
; REFERENCE/DOCKET NUMBER: 294-26
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 822-3550
; TELEFAX: (516) 822-3582
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 466 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-486-839-4

Query Match 23.8%; Score 738; DB 2; Length 466;
Best Local Similarity 34.2%; Pred. No. 4.3e-51;
Matches 152; Conservative 85; Mismatches 150; Indels 58; Gaps 11;

QY 34 RIVCYGVTSVTHKVP-YTIEDIDPFKCTHLMYGFADKIDYKTYIQVDPYQDDNHSW 92
Db 23 KLVCFYFTNWAQYRQGEARFLPKDLPSCLTHTLIYAFAGMTNHLST-----TEW 71
QY 93 -ERKGYERFNNLRKMPETLMTSLGWEYEGSEKYSMDAANTYRQFTQSVLDLFLQEVK 151
Db 72 NDTLYOEFGNGLKKNMPKLTLLAIGGNWPGTOKTDMVATANNROTTFVNSAIFRLKYS 131
QY 152 FDGLDLWDWEYVPSGR-LGNPKIDKQNTLALVRELKDAFEPHG-----YLLTAAVSPGKK 204
Db 132 FDGLDLWDWEYVPSGQ--GSPAVDKERFTLLVQDLANAFQGEAQTSGKERLLLSAAVPAGQY 190
QY 205 IDRAYDIKELNKLFDWMNVMTYDYGWENFYGHNAFLYKRPDETDELHTYFNVTMTHY 264
Db 191 VDAGYEVDKIAQNLDVNLMAVDYFHGSWEKVTGHNSPLYKQESGAAS-LNVDAVQQ 249
QY 265 YLANGATRDKLWGVPPYGRAWSIEDRSK-LKGDPAKGMSPGPGFSGEGLVSYIELCOL 324
Db 250 WLQKGTPTAKLILGMPTYGRSFTLASSSDTRVGAPATGSGTGPFTKEGMLAYYVCSW 309
QY 325 FQKEEWHIOVDEYNAPYGVNDKLVGVYDGLASISCKLAFELKELGVGMVWLENDDF 384
Db 310 KGATKORIQ-DQ--KVPYIFRDNQWGFDDVESFKTKVSYLKQKGLGGAMWALDDFA 366

Search completed: March 22, 2004, 07:03:58
Job time : 45.7332 secs


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Db 414 APTT-----STVAPGTTTTTGANPGTTPPT--SDAPNHTTTTSTTEGNGPGRTPPSG 466
Qy 485 TTTHTSETPKYTVVDGHLKCY--KEGDIPHPNIHKLVLC-----EFVNGGWWHV 535
Db 467 -----DG---PCAGRGTFVHPINPCARYICLTADTYIEFT----- 500
Qy 536 IMPCPPGTHW 545
Db 501 ---CPPGTLF 507

RESULT 2
T14075
chitinase (EC 3.2.1.14) - yellow fever mosquito
C:Species: Aedes aegypti (yellow fever mosquito)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: T14075
R:de la Vega, H.; Specht, C.A.; Liu, Y.; Robbins, P.W.
Insect Mol. Biol. 7, 233-239, 1997
A:Title: Chitinases are a multi-gene family in Aedes, Anopheles, and Drosophila.
A:Reference number: Z17872
A:Accession: T14075
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1635 <DEL>
A:Cross-references: EMBL:AF026492; NID:g2564720; PID:g2564721; PIDN:AABB1850.1
C:Genetics:
A:Gene: CHT2
A:Introns: 462/3; 524/3; 618/1; 951/3; 1151/2
C:Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 28.0%; Score 869; DB 2; Length 1635;
Best Local Similarity 34.3%; Pred. No. 4.8e-46;
Matches 196; Conservative 95; Mismatches 196; Indels 84; Gaps 18;

Qy 21 IKRDNDYSKNPM-----RIVCYVGTWSVHKVD-PYTIEDIDPFKCTHLMYFPAKIDE 73
Db 650 INKETSQDENAIESDVKVVCYTNWAWYRQGNKYLPEIDADLCTHIVIGFAVLDR 709
Qy 74 YKVTIQVDFPYQDDNHSN---EKRGYERFNNLRNLPKPELTMTISLGWYEGS-EKYSDM 129
Db 710 DRLVIK-----PHDSWADIDNFEYEVVEYKKGKVT--VAIGWNDSAGDKYSLR 759
Qy 130 AANPYRQFIQSVLDFLOEYKFDGLDLDWEYVPSRLGNPK-----IDKNYLALVRELKD 185
Db 760 VRSAAARQFIADVVAFIEKYGFGLDLDWEYVPCWQVDCKGFSDEKEGFASLVVELSQ 819
Qy 186 AFEPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDMMNVTYDYGHWENFYGHNAPLYKR 245
Db 820 AFKPKGLLSAVSPSKVVDGYDVVTLSDYMDIAVMAYDYHGQWDKKTGHVAPMYEH 879
Qy 246 PDETDELHTYFNNVTMYLNGATRDCLVNGVPFYGRAWSIEDRSKILGDPAGKMS 305
Db 880 PDDPXT---FNAFTIHWIEKGDAPRLKNGMPYNGSGFSLANKEHGLNWKTYGGGE 936
Qy 306 PGFISGEGLVSYIELCOLFOKEWHIOYDEYN-APGYNDKIVWGYDDLASISCKLAF 364
Db 937 AGESTRARGFLSYEICANIRKNKWTAVDRKRGMPYAYKGDQVSPDDQVMIRHKSEY 996
Qy 365 LKELGVSGVWWSLENDDPKHC-G-PKNPLNKVHNMINGDEKNSFECIL--GPSTTPT 421
Db 997 VKAMGLGGAMWALDLDLDFNLCDCEYPLLRINVLNRYFGPGPRCVLEKEPQREBP 1056
Qy 422 PTTTPTTTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPT 481
Db 1057 PTPRPTS-----TPPETRPRPTTISRRTTMTTITTTT---TTTRPTTTRRTSAR 1104
Qy 482 PSPTTTHTSETPKY-----TYVDGHLIKCVKEGDIHPHTNIHKLVCFEFGW 532
Db 1105 PYTIT---NVPSYQEIANEVDEFTCTDGRLP-----VHPFTDCKNYICQYK--- 1150
Qy 533 WVHIMPCCPGTIW-----CQEKLT 551
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Db 1151 -----LCPGGLYWSVDHCDWPOSTCRNKQT 1176
Qy 1151 -----LCPGGLYWSVDHCDWPOSTCRNKQT 1176

RESULT 3
A56596
chitinase (EC 3.2.1.14) - tobacco hornworm
C:Species: Manduca sexta (tobacco hornworm)
C:Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 29-Jan-1999
C:Accession: A56596
R:Kramer, K.J.; Corpuz, L.; Choi, H.K.; Muthukrishnan, S.
Insect Biochem. Mol. Biol. 23, 691-701, 1993
A:Title: Sequence of a cDNA and expression of the gene encoding epidermal and gut chitin
A:Reference number: A56596; MUID:93357793; PMID:8353525
A:Accession: A56596
A:Molecule type: mRNA
A:Residues: 1-554 <KRA>
A:Cross-references: GB:U02270; GB:S64757; NID:g406048; PID:g406049
A:Experimental source: larvae
A:Note: sequence extracted from NCBI backbone (NCBIN:136417, NCBIP:136418)
C:Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 27.0%; Score 838.5; DB 2; Length 554;
Best Local Similarity 35.4%; Pred. No. 9.2e-45;
Matches 208; Conservative 79; Mismatches 210; Indels 91; Gaps 20;

Qy 6 AILSINACIGLMMASIKRDNDYSKNPMRIVCYVGTWSVYHK-VDPYTIEDIDPFKCTHL 64
Db 3 ATLATLAVLALATAV-----QSDSRARIVCYFNSVAVYRPGVGRYGIEDIPVERCTHI 55
Qy 65 MYGFAKIDEYKTIQVDFPYQDDNHSNWEKGYERFNNLRNLPKPELTMTISLGWYEGSE 124
Db 56 IYFIFGVTGENSEVLIDPELD-----VDKNGFRNTSLRSHSPSVKFWVAVGGWAE 110
Qy 125 KYSDMAANPYRQOFQSVLDFLOEYKFDGLDLDWEYVPSGR-LGNPKIDKQNYLALVREL 183
Db 111 KYSHWAKSTRMSFIRSVVSLKKYDFDGLDLDWEYVPGADRGSFSKDKFLVLVQEL 170
Qy 184 KDAF--EPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDMMNVTYDYGHWENFYGHNA 241
Db 171 RRAPIRVKGMWELTAAPLANFRLMEGYHVPELCQELDAIHVMYSYDLRGNWAGFADVHSP 230
Qy 242 LYKPEDTDELHTYFNNVTMYLNGATRDCLVNGVPFYGRAWSIED----- 290
Db 231 LYKRPHD-QWAYEKLNVNDGLHLWEKGCPSNKLVVGPYFGRSFTLSAGNNNYGLGTFI 289
Qy 291 RSKILGDPAGKMSPPGFI SGESEGLVSYIELCOLFOKEE--WHIOYDEVYNAPYNDKI 348
Db 290 NKEAGGDPAPYTNATGP-----WAYVEICTEVKDDSGWTKWDEQKCPYAKGTQ 342
Qy 349 WVGYYDDLASISCKLAFELKELGVSGVWWSLENDDPKHCGRKPNPLNKVHNMINGDEKNS 408
Db 343 WVGVEDPRSVIEIKNWIKOKVGLGAMTWMDDFQGLCGEKNPILIKILHKMS----- 396
Qy 409 FFCILGSTTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPT 456
Db 397 -----SYTVPPPHPTENTTPEWARPPSTPDPSEGDPIPTTTAKASTTKTKTKT 449
Qy 457 TPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPT 505
Db 450 TTTTAKPQSQVIDEENDINVRPEKPEPQPEPEVEVP-PTENE-----VDSGEI 497
Qy 506 KCVKEGDIHPHTNIHKLVCFEFGWVWVHIMPCCPGTIWCCQKLT 552
Db 498 -CNSDDQDIIPDKKHCDKYWC--VNGE--AMQFSCCHGTVFNVELNVC 540

RESULT 4
A53918
chitinase (EC 3.2.1.14) precursor - braconid wasp (Chelonus sp.)
C:Species: Chelonus sp.
C:Date: 28-Jul-1995 #sequence_revision 28-Jul-1995 #text_change 21-Jul-2000
```


C;Accession: A53918
R.;Krishnan, A.; Nair, P.N.; Jones, D.
J. Biol. Chem. 269, 20971-20976, 1994
A;Title: Isolation, cloning, and characterization of new chitinase stored in active form
A;Reference number: A53918; MUID:94342256; PMID:8063715
A;Accession: A53918
A>Status: preliminary
A:Molecule type: mRNA
A;Residues: 1-483 <KB>
A;Cross-references: GI:U0422; NID:g533504; PIDN:AAA61639.1; PID:g533505
C;Keywords: glycosidase; hydrolase; polyaccharide degradation

Query Match 25.8%; Score 802; DB 2; Length 483;
Best Local Similarity 36.1%; Pred. No. 1.4e-42;
Matches 160; Conservative 89; Mismatches 162; Indels 32; Gaps 9;

QY 4 IYAILSIMACIGLWNASIKKDHNDYSKNPMRIIVCYVGTWVSYYHKVD-PYTIEDIDPFKCT 62
:
Db 6 LFVAISLVSTIAV-----ASPNNVCVFCGWSVYRQGNGKPDINGIDPTLCT 52
:
QY 63 HLMYGFPKIDEXKYITQVPDPYODDHNHSEWEKGYERFNNLRLNKPELITWISLGWYEG 122
:
Db 53 HLIIYSFVGVN--GKDVKVLDPWSDLPGN---LDGFGKFTSLRKKNPSVKIWAAGGNAG 107
:
QY 123 SEKYSDMAANPTVRQQFIQSFLDFLOSKYFDGLDLDEWPGRSGRLGNPKIDKQNYLALVRE 182
:
Db 108 SVFSPNASQAQTREAPAQNVKFLQQYQFDGFIDWEYPAQRGGSP-ADVKNMVKLCKA 166
:
QY 183 LKDAFEPHGVLTLTAAPSXGDKDRAYDIKELNKLFDMMNMVTYDYHGWENFYG-HNAP 241
:
Db 167 LKKAFOVHDYILSAANAAPTSAKSVDIAEMSQYLDFINLMTYDFHPWDGHTGMHAPP 226
:
QY 242 LYKRPEDETDELHTYTFVNNYTHMYLLNANGATRDCLVMGVPPYGRAWSIEDRSKLKGDPAP 301
:
Db 227 SASSHDSGNELK--LNVKAAKVWLQNGVPKEKLVGVGPAYGKSFILSNPSNKGLGAPVS 284
:
QY 302 GMSPPGFISGEGLSVLSIELCOLPQKEWHIQYDEYNAPYGYNDKIWGVYDDLASISCK 361
:
Db 285 GAGTAGPYTGENGLLYNEICEMOKAGDMEVQDNEKGVYAVKGNQWVSFDDLAAILAKK 344
:
QY 362 LAFLKELGVSGVMVWGLENDDFKHCGPKPLINKVHMINGDEKNSFECILQPSTT--- 418
:
Db 345 AQPIKEGLGGAMVMSIETDDFKGLGCEKYFVLKALNSVLGRGSSS-----PAETKKK 398
:
QY 419 TPTPTTTPTPTPTPTTPSPPTTP 441
:
Db 399 NNVPDDQAPPRFAEDSAPEAP 421
: :

RESULT 5
T15408
hypothetical protein C04F6.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T15408
R.;Nhan, M.
submitted to the EMBL Data Library, December 1995
A;Description: The sequence of C. elegans cosmid C04F6.
A;Reference number: Z18346
A;Accession: T15408
A;Status: preliminary; translated from GB/EMBL/DDDBJ
A:Molecule type: DNA
A;Residues: 1-617 <NHA>
A;Cross-references: EMBL:U42835; NID:g1125760; PID:g1125762; PIDN:AAA83586.1; CBSP:C04F6.3
C;Genetics:
A;Gene: CBSP.C04F6.3
A;Introns: 28/1; 66/2; 504/1

Query Match 22.7%; Score 705.5; DB 2; Length 617;
Best Local Similarity 30.2%; Pred. No. 2e-36;
Matches 178; Conservative 90; Mismatches 210; Indels 111; Gaps 19;

QY 37 CYVGTWSVYHK-VDPYTIEDIDPFCKTLMYGFADIDEYKYTIQVFDPYQDDNHNSWEKR 95

Query Match	22.0%;	Score 685;	DB 2;	Length 539;
Best Local Similarity	33.8%;	Pred. No. 3.2e-35;		
Matches 173;	Conservative 90;	Mismatches 185;	Indels 64;	Gaps 17
Qy	10	IMACIGLMAASIKRDNHNSYKNPMRIVCVGTGWSVHKVDPTYT--EDIDPFKCTHLMYG 67		
Db	4	LLLVGLL---LMLXHHGAAH--KLVCYFTNWA-FSRPGSASILPRDLDPFLCTHLVFA 57		
Qy	68	FAKIDSYKYTIQVDPYPYQDDNHNNSWEKGYERFNNLRKNPELTTMTISLGGWYSEGEKYS 127		
Db	58	FASMNNNQ--IVPKDPLD-----EKILYPEFNKLEKERNRGLKTLISVGGWNFGTSRFT 108		
Qy	128	DMAANPTYQQITQSVLDFLOEYKEDGLDLDWEVPGSLGNPKDGNPKIDKNYLALVRELKDAF 187		
Db	109	KMLSTFSNERFRVKSIVIALRTHRGDGLDFFLPGLR-GSPARDRTWTFVLEEELQAF 167		
Qy	188	EPHG-----YLLTAASVPGKDKIDRAYDIKELMKLFDMMNVMNTYDHGGWENFYGHNA 240		
Db	168	KNEAQLTMRPRLLLSAAVSGDPHVHIOKAYDARLLGRLLDFTSVLSYDLHGSWEKVTGHS 227		
Qy	241	PLYKRDETDLHTFVNNTYTHYYLNNGATREDKLVMGVPPYGRAWSIEDRSKLKLGDDPA 300		
Db	228	PLFSLPDPK-----SSAYAMSRYRQLVGPPEKLMGLPTGYRTFHLRASQNEIGAGA 281		
Qy	301	KGMSPPGFTSGEBGVLSYTELCQLFKQGEWHIQDEYVNAFYGYNDKIWYGYDDLASISC 360		
Db	282	AGPASFGYTKQAGFLAYVEVCSFVQAKRWINDQY--VPYAFKGEWGYDDAISFGY 339		
Qy	361	KLAFKLKELGVSGVMWMSLENDPFKGH-CGP-KNPLLNKVNHNINGDSKNSEFICLGPSTT 418		
Db	340	KAPFIIKREHFGGAAMVTLDDDFRGNFCTGPPFLAHTLNNLLVNDSPSS-----389		

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Qy 419 TATP-----TTATPTTTTTPSPSTTTTTPSPPTP-----TTTTPSPTTTTPSPST 466
Db 390 TSPKPFWFSTAVNSSRIGPMPPTTMDLTGILGLPGGSAVATETHRSATMTTTPRGE 449

Qy 467 TPTPT-TP-----TPAPTITPSPPTTHTS 491
Db 450 TATPTPTLSSGRRTAAPEGKTESFGKPLTS 481

RESULT 8
I38605
oviductal glycoprotein - human
C/Species: Homo sapiens (man)
C/Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 29-May-1998
C/Accession: I38605
R/Arias, E.B.; Verhage, H.G.; Jaffe, R.C.
BioI. Reprod. 51, 685-694, 1994
A/Title: Complementary deoxyribonucleic acid cloning and molecular characterization
A/Reference number: I38605; MUID:95119256; PMID:7819450
A/Accession: I38605
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-654 <RES>
A/Cross-references: EMBL:U09550; NID:4529147; PID:4529148

```

RESULT 9
A49562
cartilage glycoprotein gp39 precursor - human
NAlternate names: 3K synovial protein
C:Species: Homo sapiens (man)
C>Date: 23-Mar-1995 #sequence revision 23-Mar-

C;Accession: A49562; S10677; A33162
R;Hakala, B.E.; White, C.; Recklies, A.D.
J. Biol. Chem. 268, 25803-25810, 1993
A;Title: Human cartilage gp-39, a major secretory product of articular chondrocytes and
A;Reference number: A49562; MUID:9406458; PMID:8245017
A;Accession: A49562
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-383 <HAK>
A;Cross-references: GB:M80927; NID:G348911; PIDN:AAA16074.1; PID:G348912
R;Nyirkos, J.; Golds, E.E.
Biochem. J. 269, 265-268, 1990
A;Title: Human synovial cells secrete a 39 kDa protein similar to a bovine mammary prote
A;Reference number: S10677; MUID:90328983; PMID:2375755
A;Accession: S10677
A;Molecule type: protein
A;Residues: 22-40, 'X', 42-45 <N2>
C;Superfamily: Streptomyces chitinase chi40
C;Keywords: cartilage; extracellular protein; glycoprotein
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-383/Product: cartilage glycoprotein gp39 #status predicted <MAT>

Query Match 21.3%; Score 662; DB 2; Length 383;
Best Local Similarity 34.9%; Pred. No. 5.5e-34;
Matches 144; Conservative 81; Mismatches 136; Indels 52; Gaps 12;

QY 2 KTIYAILSIACGLMNASIKRDNDYKSNPMRIVCVGTWVYHKVDPTIED-IDPDK 60
DB 7 QTGFVLLVLLQCC-----SAYKLVCYTSWSQYREGDSCFPDLDREL 50

QY 61 CTHLMYGFADIKYKTIQVDFPQDDNHNHSEKRG---YERFNNRLKNPELTMTISLG 117
DB 51 CTHIYGFANI-----SNDHIDTWNDVTLYGMLNTLKNRNPJLKTLLSVG 97

QY 118 GWTEGSEKYSMDAANPTYRQFIQSVDLDFQEKYFGDLDDWBPYSGRLGNPKIDKQNYL 177
DB 98 GWNFGSQRFKSIANTOSRTFKSVPPFLRTHGFDGLDLAWLYPGER-----DKQHT 151

QY 178 ALVRELKDAF-----EP--HGVLTAAVSPGKIDRAYDIKGLNKLFDMNVMNTYDHGG 231
DB 152 TLIKEMAEFTKEAQPGKQKLLSALSAGKVTIDSSYDIKISQHLDFISIMTYDFHGA 211

QY 232 WENFYGNAPLYKRPDTEDELHYFNVMYTHYLNAGTRDKLVMPVPGYGAWSIEDR 291
DB 212 WRGTGTHSPFLF-RGQDASDPDRSNTDYAVMYLRLGAPASKLVMGIPTFGRSFTLAS- 269

QY 292 SKLKLGPAGKMSPPGISGEGVLSYIELCOLFOKEEMHIQYDEYNNAPYGYNDKIHWG 351
DB 270 SETGVGAPISGPGIPGRFTKEAGTLAYEICDFLRGATVHRTLGQ--QVPYATKGNQWVG 327

QY 352 YDDLASISCKLAFKELGSGVMVWSLENDDFKG-HCGP--KNPLLKNKHMI 401
DB 328 YDDQESVKSKVYLKDRQLAGAMWALDLDLDDFGSGCGQLRPLTNIAIKDAL 380

RESULT 10
S51327
heparin-binding glycoprotein 38K - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 22-Jun-1999
C;Accession: S51327
R;Shackleton, L.M.; Mann, D.M.; Millis, A.J.T.
submitted to the EMBL Data Library, January 1995
A;Description: Identification of a 38kDa heparin-binding glycoprotein (gp38k) in differ
A;Reference number: S51327
A;Accession: S51327
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-383 <SHA>
A;Cross-references: EMBL:Z47803; NID:9634097; PIDN:CAA87764.1; PID:9634098
C;Superfamily: Streptomyces chitinase chi40

Query Match 20.9%; Score 650; DB 2; Length 383;

Best Local Similarity 36.6%; Pred. No. 3.1e-33;
Matches 139; Conservative 77; Mismatches 130; Indels 34; Gaps 11;

QY 34 RIVCVYGTWSVYHKVDPTIED-IDPRKCTHLMYGFADIKYKTIQVDFPYQDDNHNH 91
DB 23 KLVCYTSWSQYREGDSCFPDLDLDFLCTHIIYSFANISNNEIDTLE-----70

QY 92 W-EKRGYERFNNRLKNPELTMTISLGWYEGSKYSMDAANPTYRQFIQSVDLDFQBY 150
DB 71 WNDVTLYDTLNTLKNRNPJLKTLLSVGNFSGQRFKSIANTOSRTFKSVPPFLATH 130

QY 151 KPDGLDLWEPYSGSLGNPKIDKQNYLALVRELKDAPEPHG-----YLLTAAVSPGKDK 204
DB 131 GPDGLDLAWISPGRR-----DKRHLLTVLTKEMAEFVREALPGTERLLLSGAVSAGKVA 184

QY 205 IDRAYDIKELNKLFDMNVMNTYDHGGWENFYGNAPLYKRPDTEDELHYFNVMYTHY 264
DB 185 IDRGYDIAIQSHLDFISLTYDFHGAWRQTTHHSPLFRGGQDASS-DRFSNADYAVSY 243

QY 265 YLNNCATRDKLVMPVPGYGAWSIEDRSLKLGDPAGKMSPPGISGEGVLSYIELCOL 324
DB 244 VLRLGAPANKLVMGIPTFGRSFTLAS-SKTDVGAPASGPGIPGRFTKEGILAYEICDF 302

QY 325 FOKEEMHIQYDEYNNAPYGYNDKIWVGYYDDLASISCKLAFKELGSGVMVWSLENDDFK 384
DB 303 LOGAT--VRPLGQGVPPVATKGNQWVGYYDDQESVKNAKYLKSRQLAGAMWTLDDDFR 360

QY 385 GH-CGP--KNPLLKNKHMI 401
DB 361 GNFCQNLRFPLTSAIKDVL 380

RESULT 11
S61551
breast-regressing protein brp39 precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
C;Accession: S61551; S61550; I48271
R;Morrison, B.W.; Leder, P.
Oncogene 9, 3417-3426, 1994
A;Title: neu and ras initiate murine mammary tumors that share genetic markers general
A;Reference number: I48271; MUID:95060797; PMID:7970700
A;Accession: S61551
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-405 <MOR1>
A;Cross-references: EMBL:X93035; NID:G1085065; PIDN:CAA63603.1; PID:G1085066
R;Morrison, B.W.
submitted to the EMBL Data Library, November 1995
A;Reference number: S61550
A;Accession: S61550
A;Molecule type: mRNA
A;Residues: 1-245, 'I', 247-330, 'H', 332-350, 'MWVALDLDLDFQGCQPKERFPLTNIAIKDALA', <MOR2>
A;Cross-references: EMBL:X93035; NID:G1085065; PIDN:CAA63603.1; PID:G1085066
A;Note: the differences at the carboxyl end are due to a frameshift error
C;Genetics:
A;Gene: brp39
C;Superfamily: Streptomyces chitinase chi40
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-405/Product: breast-regressing protein brp39 #status predicted <MAT>

Query Match 20.8%; Score 646.5; DB 2; Length 405;
Best Local Similarity 34.4%; Pred. No. 5.5e-33;
Matches 140; Conservative 73; Mismatches 129; Indels 65; Gaps 12;

QY 34 RIVCVYGTWSVYHK-VDPYTIEDIDPFKCTHLMYGFADIKYKTIQVDFPYQDDNHNH 92
DB 23 KLVCYTSWSQYREGVSGFLPDIAIQPFLCTHIIYSFANIS-----SDNMLSTW 70

QY 93 E---KRGYERFNNRLKNPELTMTISLGWYEGSKYSMDAANPTYRQFIQSVDLDFLOE 149
DB 71 EWNDSNYDKLNKLKTRNTNLKTLISVGGWKEGKRFSEIASNTERRTAFVRSVAPFLRS 130

[illegible]

```

RESULT 12
S27879
secretory protein YM-1 precursor - mouse
C/Species: Mus musculus (house mouse)
C/Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 22-Jun-1999
C/Accession: S27879
R/Chang, N.C.A.; Liu, C.H.; Chang, A.C.
submitted to the EMBL Data Library, June 1992
A/Description: Molecular characterization of a secretory protein (YM-1) transiently expressed in
A/Reference number: S27879
A/Accession: S27879
A/Molecule type: mRNA
A/Residues: 1-399 <CHA>
A/Cross-references: EMBL:M94584; NID:G202441; PID:AAB62394.1; PID:G202442
C/Superfamily: Streptomyces chitinase chi40
F/1-21/Domain: signal sequence #status predicted <SIG>
F/2-399/Product: secretory protein YM-1 #status predicted <MAT>

```

[illegible]

RESULT 13

A38221
chitinase (EC 3.2.1.14) MFI - nematode (Brugia malayi)
C/Species: Brugia malayi
C/Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
C/Accession: A38221
R/Fuhrman, J.A.; Lane, W.S.; Smith, R.F.; Piessens, W.F.; Perler, F.B.
Proc. Natl. Acad. Sci. U.S.A. 89, 1548-1552, 1992
A/Title: Transmucosal-blocking antibodies recognize microfilarial chitinase
A/Reference number: A38221; MUID:92179220; PMID:1542646
A/Accession: A38221
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: nucleic acid; protein
A/Residues: 1-504 <FUH>
A/Cross-references: GB:W37689; NID:g156063; PIDN:AAA27854.1; PID:g156064
A/Note: sequence extracted from NCBI backbone (NCBIP:85345)
C/Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 19.5%; Score 604.5; DB 2; Length 504;
Best Local Similarity 30.1%; Pred. No. 3e-30;
Matches 156: Conservative 86; Mismatches 208; Indels 69; Gaps 17;

```

Qy 37 CYVGWVSVTHKVD--PYTTIEDDPFCKTLMGPKAIDBYKYTIQVPDYO--DNHNSWEK 94
Db 27 CYYTNWAQYRDGEGRFLPONTINGLICHTILYAFKAVDE---LGDSPFFEWNDTEJWSK 82
Qy 95 RGYERNNILRNKPBLTTMI SLGWYEGSEKYS DWAANPTYROOFIOSVLDFLOEYKFOD 154
Db 83 GMYSAVTKLRETPNGUKLLSYGGYNFGSALFTGIASAKQTERFIKSATAFURKNNFOD 142
Qy 155 LLDLDWEYP--GSRLGNPKDKONYIALVALVELXDAPEPHGYLLTAAVSPGKOKIDRAYDIKE 213
Db 143 FDLDWEPYGVGAEBEAKLVEMKTRAFVEZAKTSKQR--LLLTAAVSAGKTIDGSIYNVES 201
Qy 214 LNLKLPDMNVMTYDYHGOWENFYGHNAPLYKRPPDETDELHTYFNUNYTMHYLLNANGATR 273
Db 202 LGKNFDLLFLMSYDLHGSEKXNDVLHGKLIHPTKGESGI--GIFNTEPAADYWSKGMPE 266
Qy 274 KLVMGVFPFGRAWSTEDRSKULGPDPKMGSPPOFISGEEBGLSYIELQLQFQKEWHIQ 333
Db 261 KIIIGIPMAQGMTLDNPSETAIGAASRRPSASKTNPAGGTASYBEICKYLKGGKETV 320
Qy 334 YDBEYNAPGYNDKIWVGVDLLASISKLAFLKELGYSGVMVWLENDDFKG--HCGP-KN 391
Db 321 HQBGVGA--YMWKGOMYGYDNEETIRIKMKWLKSKYGGAIFWALDDFDTFKGSCGKPY 379
Qy 392 PLLNKVHNMDGKNSPECILGSPTTTTPTTTPTTTPTTTPTTPTTPTTPTTPTTPTTPTTPT 455
Db 380 PLLNALISSELGESEN-----PLITTEESISETEAYETDETEE 418
Qy 452 TTPSPTTTTPTTPTTPTTPTAPTSTSTPTTTEHTSETPKYTYY---VDGHLIKC 507
Db 419 -----TSETAYDTD----ETEETSET-BATTYDTDTEGO--EC 455
Qy 508 -YKEGDIPIPTNIHKYLCEFVNGGWVHHIMPCPPGTIW 545
Db 452 PERDGIFFRPTCHLFIOQ---ANNIAYWQCATTFF 486

```

RESULT 14

D83764
chinese: BH0916 [imported] - Bacillus halodurans (strain C-125)
C/Species: Bacillus halodurans
C/Date: 01-Dec-2000 #text_change 01-Dec-2000 #text_change 15-Jun-2001
C/Accession: D83764
R/Takam, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; F
Nucleic Acids Res. 28, 4317-4331, 2000
A/Title: Complete genome sequence of the alkaliphilic bacterium Bacillus ha
A/Reference number: AB3650; MUID:20512582; PMID:11058432

A;Status: preliminary
A;Molecule type: DNA

A;Residues: 1-599 <STO>

A;RESIDUES: 1-399 <SIO>
A;CROSS-references: GB:AP001510; GB:BA000004; NID:q10173440; PIDN:BA04635.1; GSPDB:GN00

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 22, 2004, 06:31:13 ; Search time 21.2868 Seconds
(without alignments)
1357.597 Million cell updates/sec

Title: US-09-662-293-18

Perfect score: 31.07

Sequence: 1 MKTIYALISIMACIGLNNAS.....IMCPPPTIWCQEKLTIGE 555

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	838.5	27.0	554	1	CHIT MANSE
2	738	23.8	466	1	CHT1 HUMAN
3	734.5	23.6	473	1	CHIA MOUSE
4	723	23.3	508	1	CHIL DROME
5	708.5	22.8	476	1	Q9W5U3 drosophila
6	705.5	22.7	617	1	CHIT CAEEL
7	696.5	22.4	527	1	Q9B9P6 homo sapien
8	685.5	22.1	537	1	Q28990 sus scrofa
9	685	22.0	539	1	Q28042 bos taurus
10	680	21.9	381	1	Q28542 ovis aries
11	680	21.9	381	1	Q61362 mus musculus
12	680	21.9	721	1	Q60557 mesocricetu
13	668	21.5	678	1	Q62010 mus musculus
14	662	21.3	383	1	Q12889 homo sapien
15	654.5	21.1	623	1	P36222 homo sapien
16	630	20.3	390	1	P36718 papio anubi
17	611.5	19.7	396	1	Q15782 homo sapien
18	604.5	19.5	504	1	Q9d7q1 mus musculus
19	576	18.5	458	1	P29030 brugia mala
20	561	18.1	699	1	Q9W5U2 drosophila
21	411	13.2	423	1	P20333 bacillus ci
22	410.5	13.2	423	1	P48827 trichoderna
23	407.5	13.1	563	1	P32470 aphanocladi
24	384	12.4	820	1	P07254 serratia ma
25	377.5	12.1	550	1	P32823 alteromonas
26	360.5	11.6	551	1	Q10363 orgyia pseu
27	353	11.4	499	1	P41684 autographa
28	341	11.0	619	1	P11797 serratia ma
29	339.5	10.9	427	1	P36909 streptomyce
30	326	10.5	610	1	P54196 coccidioid
31	280	9.0	1046	1	P11220 streptomyce
32	266.5	8.6	474	1	P96156 vibrio furn
33	259	8.3	5179	1	P19275 thermoprote
					Q02817 homo sapien

ALIGNMENTS

RESULT 1

CHIT MANSE

ID	CHIT MANSE	STANDARD	PRT	554 AA
DT	01-JUN-1994 (Rel. 29, Created)			
DT	01-JUN-1994 (Rel. 29, Last sequence update)			
DT	15-MAR-2004 (Rel. 43, Last annotation update)			
DE	Endochitinase precursor (EC 3.2.1.14).			
OS	Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).			
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;			
OC	Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Sphingioidea;			
OC	Sphingidae; Sphinginae; Manduca.			
OX	NCBI_TaxID=7130;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=93357793; PubMed=8353525;			
RA	Kramer K.J., Corpuz L., Choi H.K., Muthukrishnan S.;			
RT	"Sequence of a cDNA and expression of the gene encoding epidermal and			
RT	gut chitinases of Manduca sexta.";			
RL	Insect Biochem. Mol. Biol. 23:691-701(1993).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=97215580; PubMed=9061927;			
RA	Choi H.K., Choi K.H., Kramer K.J., Muthukrishnan S.;			
RT	"Isolation and characterization of a genomic clone for the gene of an			
RT	insect molting enzyme, chitinase.";			
RL	Insect Biochem. Mol. Biol. 27:37-47(1997).			
CC	!- FUNCTION: Digest chitin in the exoskeleton during the molting			
CC	process.			
CC	!- CATALYTIC ACTIVITY: Hydrolysis of the 1,4-beta-linkages of N-			
CC	acetyl-D-glucosamine polymers of chitin.			
CC	!- SUBCELLULAR LOCATION: Secreted.			
CC	!- TISSUE SPECIFICITY: Epidermis and gut.			
CC	!- DEVELOPMENTAL STAGE: High levels seen in the epidermis on day 0,			
CC	but rapidly disappears and is undetected on days 1-4 of fifth a			
CC	instar. It reappears on day 5 and peaks on day 7 after which a			
CC	rapid decline is seen. In the gut is detected on day 6 with lower			
CC	levels seen on days 0, 7 and 8.			
CC	!- SIMILARITY: Belongs to chitinase class II (family 18 of glycosyl			
CC	hydrolases).			
CC	!- SIMILARITY: Contains 1 chitin-binding type-2 domain.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
DR	EMBL; U02270; AAC04924.1; -			
DR	EMBL; I49234; AAB53952.1; -			
DR	PIR; A56596; A56596.			
DR	InterPro; IPR002557; Chitin bind_Pera.			
DR	InterPro; IPR001223; Glyco_hydro_18.			
DR	InterPro; IPR001579; Glyco_hydro_18AS.			

Q62635 rattus norv
Q05049 xenopus lae
O10341 orgyia pseu
P10667 xenopus lae
P22533 caldocellum
P14518 zea mays (m
Q06885 dictyosteli
P47179 saccharomyc
P22699 dictyosteli
P09805 kluyveromyc
P24152 sorghum bic
P02840 drosophila

```
DR Pfam; PF01607; CBM_14; 1.
DR Pfam; PF00704; Glyco_hydro_18; 1.
DR ProDom; PD000471; Glyco_hydro_18; 1.
DR SMART; SM00494; ChitD2; 1.
DR SMART; SM00636; Glyco_18; 1.
DR PROSITE; PS00940; CHIT_BIND_II; 1.
DR PROSITE; PS01095; CHITINASE_18; 1.
DR Hydrolase; Glycosidase; Chitin degradation; Chitin-binding; Signal;
KW Glycoprotein.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 554 ENDOCHITININASE.
FT DOMAIN 396 453 SER/THR-RICH.
FT DOMAIN 495 553 CHITIN-BINDING TYPE-2.
FT ACT_SITE 146 146 PROTON DONOR (BY SIMILARITY).
FT CARBOHYD 85 85 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 303 303 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 407 407 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 545 545 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 554 AA; 62203 MW; 3989D756C96CD490 CRC64;

Query Match 27.0%; Score 838.5; DB 1; Length 554;
Best Local Similarity 35.4%; Pred. No. 6.3e-39;
Matches 208; Conservative 79; Mismatches 210; Indels 91; Gaps 20;

QY 6 ALLSTMAGIGLGNASIKRHDNDYKSNPMRIYCVYGVTSVYHK-VDEYTIEDIDPFKCTHL 64
DB 3 ATLALVALATAV-----QDSRARIVCYFSNMAVYRPGVGRYGIEDIPVEKCTHI 55
QY 65 MYGFAKIDYKYTIQVDPYQDDNHNWKEKGYRFRNNLRKNPELMTISLGGWYEGSE 124
DB 56 IYSGIVTEGSEVLIIIDPELD-----VDKNGFENFTSLRSHSPVSKFMVAVGWAAGSS 110
QY 125 KYSDMAANPTVROQFIQSVLDFLOEYKPDGLDLWEYPSGR-LGNPKIDKQNYALVREL 183
DB 111 KYSHVAQKSTRMSFIRSWFLKKYKPDGLDLWEYPSGAADRGSPSDKFLYLVOEL 170
QY 184 KDAP--EHEGYLLTAASVPGKDKIDRAYDIKELNKLDPMMWVYDYHGGWENFYGNAP 241
DB 171 RRAFTRVGKGWELTAAPLANFRMLMEGYHVPCLQELDAIHVMYDILRGNWAGFADHSP 230
QY 242 LYKRDEDELTHTYNNVNTWHYLLNNGATDKLVMPVFPFYGRAWSIED----- 290
DB 231 LYKRPHD-QWAVEKLVNDGLHLWEKCPKCNKLVGLIPFYGRSFTLSAGNNYGLGTFI 289
QY 291 RSKLGLDPAKMSPPGISGEEVLSYIELCOLFKQEE--WHIQDYEVNAPYGYNDKI 348
DB 290 NKEAGGDPAPYATNATG-----WAYEICTEVDKDDSGTWKWDQKCPYAKGTQ 342
QY 349 WGYDDLASISCKLAFELKELGVSGVMWVSLNDFKGCGRPNLKNVNMINGDEKNS 408
DB 343 WGYEDPRSVEIKMNIQKQYLGANTWAIIDMDDFQGLCGEKNPLIKLHKRMS----- 396
QY 409 FECILGPSTTPTPTTPTTPTT-----TTPTTPS-----PTPTTPSTTPTTPTSP 456
DB 397 -----SYTVPPPHPTNTTTPPEWARPSPSPSEGDPIPTTTAKPASTTKTIVKTT 449
QY 457 TPTTTPSPFT-----PTP-TTPTPAPTSTPSPTTTEHTSETPKYTTTVVDGHLI 505
DB 450 TTTAKPQGVDEENDINVRPEPPEPQPEVEVP-PTENE-----VDGSEI 497
QY 506 KYCEGD-IPHPTNTHKLVCFVNGVNGWVHIMPCFPGTIWCQEKLTIC 552
DB 498 -CNSQDDYIPDKKHCDKYRWC--VNGE--AMQFSQHGTVFVNLNVC 540

RESULT 2
ID CHIT1 HUMAN
AC Q13231; OSH3V8;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Chitotriosidase 1 precursor (EC 3.2.1.14) (Chitinase 1).
```

```
GN CHIT1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), FUNCTION, AND SUBCELLULAR
RP LOCATION.
RC TISSUE=Macrophage;
RX MEDLINE=96064695; PubMed=7592832;
RA Boot R.G., Renkema G.H., Strijland A., van Zonneveld A.J.,
RA Aerts J.M.F.G.;
RT "Cloning of a cDNA encoding chitotriosidase, a human chitinase
RT produced by macrophages.";
RL J. Biol. Chem. 270:26252-26256 (1995).
RN [2]
RP SEQUENCE OF 22-42 AND 178-198, FUNCTION, AND TISSUE SPECIFICITY.
RX MEDLINE=95138187; PubMed=7836450;
RA Renkema G.H., Boot R.G., Mulijers A.O., Donker-Koopman W.E.,
RA Aerts J.M.F.G.;
RT "Purification and characterization of human chitotriosidase, a novel
RT member of the chitinase family of proteins.";
RL J. Biol. Chem. 270:2198-2202 (1995).
RN [3]
RP POLYMORPHISM, AND DESCRIPTION OF ISOFORM 3.
RX MEDLINE=98421482; PubMed=9748235;
RA Boot R.G., Renkema G.H., Verhoek M., Strijland A., Bliet J.,
RA de Meulener T.M.A.M.O., Mannens M.M.A.M., Aerts J.M.F.G.;
RT "The human chitotriosidase gene. Nature of inherited enzyme
RT deficiency.";
RL J. Biol. Chem. 273:25680-25685 (1998).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 22-386 IN COMPLEX WITH
RP CHITBIOSIDE AND ALLOSAMIDIN.
RX MEDLINE=22095530; PubMed=11960986;
RA Fusetti F., von Moeller H., Houston D., Rozeboom H.J., Dijkstra B.W.,
RA Boot R.G., Aerts J.M.F.G., van Aalten D.M.F.;
RT "Structure of human chitotriosidase. Implications for specific
RT inhibitor design and function of mammalian chitinase-like lectins.";
RL J. Biol. Chem. 277:25537-25544 (2002).
CC -I- FUNCTION: Degrades chitin and chitotriose. May participate in the
CC defense against nematodes and other pathogens. Isoform 3 has no
CC enzymatic activity.
CC -I- CATALYTIC ACTIVITY: Hydrolysis of the 1,4-beta-linkages of N-
CC acetyl-D-glucosamine polymers of chitin.
CC -I- SUBUNIT: Monomer.
CC -I- SUBCELLULAR LOCATION: Secreted. A small proportion is lysosomal.
CC -I- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=1;
CC IsoId=Q13231-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q13231-2; Sequence=VSP_008631, VSP_008632;
CC Name=3;
CC IsoId=Q13231-3; Sequence=VSP_008633;
CC Note=Duplication of 24 bp in exon 10 leads to the use of a
CC cryptic splice site. The normal splice site is still present but
CC not used.
CC -I- TISSUE SPECIFICITY: Detected in spleen. Secreted by cultured
CC macrophages.
CC -I- POLYMORPHISM: A 24 bp duplication in exon 10 leads to the
CC activation of an alternative splice site and the production of an
CC inactive protein. About 6% of the population are deficient for
CC CHIT1 activity, while 35% are carriers and show reduced enzyme
CC levels. PEOPLE with CHIT1 deficiency appear perfectly healthy.
CC -I- MISCELLANEOUS: Patients with type 1 Gaucher disease (GD 1)
CC [MIM:230800] have very high plasma levels of CHIT1, and this can
CC be used as diagnostic aid and to evaluate the success of
CC treatment. Successful therapy brings the CHIT1 activity levels
CC back to normal.
CC -I- SIMILARITY: Belongs to chitinase class II (family 18 of glycosyl
CC hydrolases).
CC -I- SIMILARITY: Contains 1 chitin-binding type-2 domain.
```

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CC	EMBL; U29615; AAC50246.1; ?.
CC	EMBL; U62662; AAG10644.1; -.
DR	PDB; LGUV; 31-JAN-02.
DR	PDB; ILG1; 18-SEP-02.
DR	PDB; ILG2; 18-SEP-02.
DR	PDB; ILQ0; 29-JUL-03.
DR	MIM; G60031; ?.
DR	GO; GO:0005615; C:extracellular space; TAS.
DR	GO; GO:0004568; F:chitinase activity; TAS.
DR	GO; GO:0009617; P:response to bacteria; TAS.
DR	GO; GO:0009613; P:response to pest/pathogen/parasite; TAS.
DR	InterPro; IPR002557; Chitin bind PerA.
DR	InterPro; IPR001223; Glyco_hydro_18.
DR	InterPro; IPR001579; Glyco_hydro_18AS.
DR	Pfam; PF01607; CBM_14; 1.
DR	Pfam; PF00704; Glyco_hydro_18; 1.
DR	ProDom; PD000471; Glyco_hydro_18; 1.
DR	SMART; SM00494; ChtBD2; 1.
DR	SMART; SM00636; Glyco 18; 1.
DR	PROSITE; PS50940; CHIT_BIND_I; 1.
DR	PROSITE; PS01095; CHITINASE_18; 1.
KW	Carbohydrate metabolism; Chitin degradation;
KW	Polysaccharide degradation; Hydrolase; Glycosidase; Chitin-binding;
KW	Signal; Alternative splicing; 3D-structure.
FT	SIGNAL 1 21
FT	CHAIN 22 466
FT	DOMAIN 417 466
FT	ACT_SITE 140 140
FT	DISULFID 26 51
FT	DISULFID 307 370
FT	VARSPLIC 386 387
FT	VARSPLIC 388 466
FT	VARSPLIC 344 372
FT	VARSPLIC 466 AA; 51681 MW; B4312D1E885E386D CRC64;
FT	SEQUENCE

Query Match	23.8%; Score 738; DB 1; Length 466;
Best Local Similarity	34.2%; Pred. No. 1.6e-33;
Matches 152; Conservative 85; Mismatches 150; Indels 58; Gaps 11;	

QY	34 RIVCVGTWSYHKVDP-YTTEDIDPKCTHLMYGFPAKIDBYKYTIQVDFPDYDDNHSW 92
Db	::::: : : : : : : : : : : : : : : : : :
QY	23 KLVCFYTNWAQYRGAEFLFKDLDPISLCTHLIYAFAGMTNHQLST-----TEW 71
QY	93 -EKGRYEFNNLRLNKPETLMI SILGWYESESKYSDMAANFTVRQOFLOSILDFLEQYK 151
Db	: :
QY	72 NDETLYQBFNLKKQNPKLTLLLAIGWNFGTQTFTDMVTANNRQTFVNARFRURKYS 131
QY	152 FDGLDLWEYEGSLGNPKIDKNYLALVRELKDAFEFHG-----YLITAAVSPPGDK 204
Db	: :
QY	132 FDGLDLWEYEGSQ-GSPAVDKERFTTLVDLANAQEAQTSCKERLLLSAAVPAGQTY 190
QY	205 IDRAYDIKELNFLDWNNWTYHYHGWFNYGHNAFLYKRDETDDELHTFYFNNTMYH 264
Db	: :
QY	191 VDAGEYVDKIAQNTDFNLMAYPFHGSWEKVYTGNSPLYKRQESGAAS-LNVDAVQQ 249
QY	265 YLNGATRDKLVMGVPFPGRAWSETDSKLLGDPAKGMSPPGFISCEEGVLVIELCQL 324
Db	: :
QY	250 WLQGTPTASKUILGNPTYGRSFTLIASSSDTRVGAPATGSGTPGPTKEGGMLAYEVCSW 309
QY	325 FQBEWHIQYDEYNAPYGNDKIWWGVYDDLASTCKLAFKLKELIGSVGMVWGLENDFFK 384

[illegible]

```

DR PROSITE; PS00940; CHIT_BIND II; 1.
DR PROSITE; PS01095; CHITINASE 18; 1.
KW Carbohydrate metabolism; Chitin degradation;
KW Polysaccharide degradation; Hydrolase; Glycosidase; Chitin-binding;
KW Signal; Alternative splicing.
FT SIGNAL 1 21 BY SIMILARITY.
FT CHAIN 22 476 ACIDIC MAMMALIAN CHITINASE.
FT DOMAIN 427 476 CHITIN-BINDING TYPE-2.
FT DOMAIN 415 420 POLY-SER.
FT ACT_SITE 140 140 BY SIMILARITY.
FT DISULFID 26 51 BY SIMILARITY.
FT DISULFID 307 372 BY SIMILARITY.
FT VARSPIC 1 161 Missing (in isoform 3).
FT VARSPIC 1 108 Missing (in isoform 2).
FT CONFLICT 339 339 I -> V (IN REF. 1).
FT CONFLICT 432 432 V -> G (IN REF. 1).
SQ SEQUENCE 476 AA; 52271 MW; 92B27BAD2F7EB4CC CRC64;

Query Match 22.8%; Score 708.5; DB 1; Length 476;
Best Local Similarity 35.9%; Pred. No. 6.4e-32;
Matches 149; Conservative 75; Mismatches 154; Indels 37; Gaps 10;

QY 34 RIVCVGVGWSVYHK-VDPYTTIEDIDPFKCTHLMYGFADKIDYKYTIQVDFPYQDDNHSW 92
DB 23 QLTCTFTNWAQYRGLGRFMDNIDPCLCTHLIVAFAGRQNNETT-----IEW 71

QY 93 -EKRGYERFNLRKLNPELTMTISLGWYEGSEKYSDMAANPTYRQOFIQSVLDFLOEYK 151
DB 72 NDVTLYQAFNGKKNKNSQLTKLLAIGGNWFTAFPTANVSTPENRQTFITSVIKFLQYE 131

QY 152 FDGLDWEYFGSLGNPKIDQNYLALVRELKDAFPHG-----YLTAASVSPGKDK 204
DB 132 FDGLDWEYFGSR-GSPDQKHLFTVLVQSMREAFQEAQINKPLMTAAVAAGISN 190

QY 205 IDRAYDIKELNKLFDWMNVMYDYHGGWENFYGNAPLYKRPDSTDLHYFYFNVMYHY 264
DB 191 IQSGYEIPQLSQYLDYHWMYDLEHSGWEGTGENSPLYKYPTDTGS-NAYLNVYVMYNY 249

QY 265 YLNGATKDLVMGVFFYGRAWSIEDRSKLGIDPAKGMSPPGFISGEGVLSVIELCOL 324
DB 250 WKDNGAPAEKLVIFGPTTYGHNFILSNPNTGIGAPTSGAGPAGPYAKESGIWAYEIC-T 308

QY 325 FQKESEWHIQDYENYAPGYNDKLVGYDDILASISCKLAFKELGVSGVMVWMSLENDFFK 384
DB 309 FLKNGATQGWADAPQVEVPAYQGVNMGVYDNKISFDIKAQWLKHNKFGGMWALDLDFT 368

QY 385 G-HGCP-KNPLLNKVNHNMGDEKNSFECILGSPSTPTPTPTPTPTPTPTPTPTPTPS 437
DB 369 GTFCNQGRFLI-----STLKALGLQASCTAPAQPIETAPSGS 411

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RESULT 6

```

ID CHIT_CABEL STANDARD; PRT; 617 AA.
AC Q11174; O17321;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Probable endochitinase (EC 3.2.1.14).
GN CHT-1 OR C04F6.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelecorinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Nham M.;
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 62-178 FROM N.A.

```

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RX MEDLINE=98324849; PubMed=9662472;
RA de la Vega H., Specht C.A., Liu Y., Robbins P.W.;
RT "Chitinases are a multi-gene family in Aedes, Anopheles and
RT Drosophila.";
RL Insect Mol. Biol. 7:233-239 (1998).
CC -I- CATALYTIC ACTIVITY: Hydrolysis of the 1,4-beta-linkages of N-
CC acetyl-D-glucosamine polymers of chitin.
CC -I- SIMILARITY: Belongs to chitinase class II (family 18 of glycosyl
CC hydrolases).
CC -I- SIMILARITY: Contains 2 chitin-binding type-2 domains.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL; U42835; AA893586.1; -
DR EMBL; AF026152; AA881847.1; -
DR PIR; T15408; T15408.
DR PIR; T37249; T37249.
DR WormPep; C04F6.3; CE03923.
DR InterPro; IPR002557; Chitin_bind_Pera.
DR InterPro; IPR001223; Glyco_hydro_18.
DR InterPro; IPR001579; Glyco_hydro_18AS.
DR Pfam; PF01607; CEM_14; 2.
DR Pfam; PF00704; Glyco_hydro_18; 1.
DR ProDom; PD000471; Glyco_hydro_18; 1.
DR SMART; SM00494; ChtB2; 2.
DR SMART; SM00636; Glyco_18; 1.
DR PROSITE; PS00940; CHIT_BIND II; 2.
DR PROSITE; PS01095; CHITINASE 18; 1.
KW Hydrolase; Glycosidase; Chitin degradation; Chitin-binding; Repeat.
FT DOMAIN 478 534 CHITIN-BINDING TYPE-2 1.
FT DOMAIN 563 617 CHITIN-BINDING TYPE-2 2.
FT ACT_SITE 179 179 PROTON DONOR (BY SIMILARITY).
FT DOMAIN 435 478 THR-RICH.
FT CONFLICT 138 138 W -> C (IN REF. 2).
FT CONFLICT 163 165 ITF -> TTS (IN REF. 2).
FT CONFLICT 176 176 I -> L (IN REF. 2).
SQ SEQUENCE 617 AA; 66857 MW; DDALD2AAAC0ES4DA CRC64;

Query Match 22.7%; Score 705.5; DB 1; Length 617;
Best Local Similarity 30.2%; Pred. No. 1.3e-31;
Matches 178; Conservative 90; Mismatches 210; Indels 111; Gaps 19;

QY 37 CYVGVWSVYHK-VDPYTTIEDIDPFKCTHLMYGFADKIDYKYTIQVDFPYQDDNHSWEKR 95
DB 57 CYFTNWAQYRQGRKFPVBDYTPGLCTHLIFAGWNA-DYTVRAYDP--ADLPNDWAGE 113

QY 96 G-YERNRLRNKLNPELTMTISLGWYEGSEKYSDMAANPTYRQOFIQSVLDFLOEYKPG 154
DB 114 GMYRVNKLKVTDTQLKTLISFGWSFGTALPQGMASASRKFVIDSAITVRTWTFDG 173

QY 155 LLDLWEYFGSLGNPKIDQNYLALVRELKDAFPHG-----YLTAASVSPGKDKIDR 207
DB 174 IDIDWEYPSG-----ATDMANYVALVKEKLAACEASEAGSTGKDRLLVTAAGAATIDA 228

QY 208 AYDIKELNKLFDWMNVMYDYHGGWENFYGNAPLYKRPDSTDLHYFYFNVMYHYLN 267
DB 229 GYDIPNLAFNDFPILLMSYDFFGAWASLVGFNSPLYATTELPAEWNGW-NVDSSARYNQ 287

QY 268 NGATRKLVGMVFFYGRAWSIEDRSKLGIDPAKGMSPPGFISGEGVLSVIELCOLFOK 327
DB 288 KGMPEKILVGMPTYGRGWTNNASAINPFGTSGSPAKITQYVQ-EAGVAYFECEMLAN 346

QY 328 EWHIQDYENYAPGYNDKLVGYDDILASISCKLAFKELGVSGVMVWMSLENDFFKHC 387
DB 347 GATR-YWDSQSQVPLVQGNQWMSYDDESFANKYAYVYKREGYGGAFVWTLDFDFFNAGC 405

QY 388 GPKN-----FLNKNVHNMGDEKNSFECIL---GFSTTPTT-----PTTPTTPT 429

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DR	PIR; S57197; S57197.	RC	TISSUE-Oviduct;
DR	InterPro; IPR001223; Glyco_hydro_18.	RX	MEDLINE=95269691; PubMed=7750470;
DR	InterPro; IPR001579; Glyco_hydro_18AS.	RA	Desouza M.M., Murray M.K.;
DR	Pfam; PF00704; Glyco_hydro_18; 1.	RT	"An estrogen-dependent secretory protein, which shares identity with
DR	ProDom; PD000471; Glyco_hydro_18; 1.	RT	chitinases, is expressed in a temporally and regionally specific
DR	SMART; SM00636; Glyco_18; 1.	RT	manner in the sheep oviduct at the time of fertilization and embryo
DR	PROSITE; PS01095; CHITINASE_18; FALSE_NEG.	RL	development";
KW	Glycoprotein; Fertilization; Signal.	RL	Endocrinology 136:2485-2496(1995).
FT	NON_TER 1	RN	(2)
FT	SIGNAL <1 18	RP	SEQUENCE OF 10-539 FROM N.A.
FT	CHAIN 19 537	RC	STRAIN=Mexino; TISSUE=Oviduct;
FT	CARBOHYD 399 399	RX	MEDLINE=96329120; PubMed=8726871;
FT	SEQUENCE 537 AA; 59617 MW; CFCDE6F0212D791 CRC64;	RA	Marshall J.T.A., Nancarrow C.D., Brownlee A.G.;
Qy	Query Match 22.1%; Score 685.5; DB 1; Length 537;	RT	"Cloning and sequencing of a cDNA encoding an ovine
Db	Best Local Similarity 33.3%; Pred. No. 1.3e-30;	RT	ovine-associated oviductal protein.";
Db	Matches 173; Conservative 95; Mismatches 183; Indels 69; Gaps 19;	CC	Reprod. Fertil. Dev. 8:305-310(1996).
Qy	10 IMACIGLNASIKRDNDYKSNPMRIVCYGVTSVHKVDPTI--EDIDPFKCTHLMYG 67	CC	in the fertilization process and/or early embryonic development.
Db	1 LLLCVGLL--LVLRKHGDAH--KLVCYFTNWA-FSRPGFASILPRDLDPFLCTHLEVA 54	CC	in the fertilization process and/or early embryonic development.
Qy	68 FAKIDEVYKTIQVDPDQDNHNSWEKRGYERFNRLKKNPELTMTLSLGGWYEGSEKYS 127	CC	in the fertilization process and/or early embryonic development.
Db	55 FASMSNNQ--IVPKDPLD-----EKILYFENFKLERNRGLKLLSIGWNFGIVRFT 105	CC	in the fertilization process and/or early embryonic development.
Qy	128 DMAANPTYROOFTQSVLDFLOEYKFDGLDMEYPGSRGLGNPKIDKONVIALVRELKDAF 187	CC	in the fertilization process and/or early embryonic development.
Db	106 TMLSTFNRERFVSSVIALRTHGFDGLDLFFLYPGLR-GSPARDRTWTFVLEELLQAF 164	CC	in the fertilization process and/or early embryonic development.
Qy	188 EPHG-----YLLTAASVFGKIDRAYDIKELNKLFLDMNVMYDYHGGWENFYGHNA 240	CC	in the fertilization process and/or early embryonic development.
Db	165 KNEAQLTWPRPELLLSAAVGDPHVQKAYEARLLGRLLDISVLSDYHLSWEKVTGHNS 224	CC	in the fertilization process and/or early embryonic development.
Qy	241 PLYKRPDETLHYFNVMYTHYLLANGATROKLVNGVFPYGRAMSIDRSKLGDPDA 300	CC	in the fertilization process and/or early embryonic development.
Db	225 PLFLSLPGDPK-----SSAYAMNYRQLGVPEPKLMLGLTYGTFHLLKASQNELRAQA 278	CC	in the fertilization process and/or early embryonic development.
Qy	301 KGMSPPGFISGEGVLSVIELCOLFOKEWHIOQDEYVNPAPYGYNDKIWGYDDLASISC 360	CC	in the fertilization process and/or early embryonic development.
Db	279 VGPASPGKYTKQAGFLAYEICCVRRAKRWINDQY--VPYAFKGEWGYDDAISFGY 336	CC	in the fertilization process and/or early embryonic development.
Qy	361 KLAFELKELGSGVMVMSLENDDFKGH-CGP-KNPLLNKVNMMINGDEKNSFECILGPSTT 418	CC	in the fertilization process and/or early embryonic development.
Db	337 KAPFKRHFEGAMVWTLDDLDFGFGCGTGFPLVHLNLLVNDFFSS-----386	CC	in the fertilization process and/or early embryonic development.
Qy	419 TPTP-----TTTTPTTPTTPTTPTTPTTPTT-----TTTTPTTPTTPTTPTT 466	CC	in the fertilization process and/or early embryonic development.
Db	387 TSPKFWFSTAVNSRIGPMPMTWTRDLTTLGLILPGGEAVATETHRKSETMTITPKGE 446	CC	in the fertilization process and/or early embryonic development.
Qy	467 TPTPT-TP-----TPATTSTPSP-----TTTTHTSETP 494	CC	in the fertilization process and/or early embryonic development.
Db	447 IATPTPTPLSGRHTAAPEKGTESPGKPLATVGLAVSP 486	CC	in the fertilization process and/or early embryonic development.
RESULT 9		CC	in the fertilization process and/or early embryonic development.
OGP_SHEEP	STANDARD; PRT; 539 AA.	CC	in the fertilization process and/or early embryonic development.
AC	Q28542; Q28543;	CC	in the fertilization process and/or early embryonic development.
DT	01-NOV-1997 (Rel. 35, Created)	CC	in the fertilization process and/or early embryonic development.
DT	01-NOV-1997 (Rel. 35, Last sequence update)	CC	in the fertilization process and/or early embryonic development.
DT	30-MAY-2000 (Rel. 39, Last annotation update)	CC	in the fertilization process and/or early embryonic development.
DE	Oviduct-specific glycoprotein precursor (Oviductal glycoprotein)	CC	in the fertilization process and/or early embryonic development.
DE	(Oviductin) (Estrogen-dependent oviduct protein) (Estrus-associated	CC	in the fertilization process and/or early embryonic development.
DE	oviductal glycoprotein) (OEGP).	CC	in the fertilization process and/or early embryonic development.
GN	OVID1 OR OGP.	CC	in the fertilization process and/or early embryonic development.
OS	Ovis aries (Sheep).	CC	in the fertilization process and/or early embryonic development.
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	CC	in the fertilization process and/or early embryonic development.
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;	CC	in the fertilization process and/or early embryonic development.
OC	Bovidae; Caprinae; Ovis.	CC	in the fertilization process and/or early embryonic development.
OX	NCBI_TaxID=9940;	CC	in the fertilization process and/or early embryonic development.
RN	[1]	CC	in the fertilization process and/or early embryonic development.
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 22-39.	CC	in the fertilization process and/or early embryonic development.

Query Match 22.0%; Score 685; DB 1; Length 539;
Best Local Similarity 33.8%; Pred. No. 1.4e-30;
Matches 173; Conservative 90; Mismatches 185; Indels 64; Gaps 17;

Qy 10 IMACIGLNASIKRDNDYKSNPMRIVCYGVTSVHKVDPTI--EDIDPFKCTHLMYG 67
Db 4 LLLCVGLL--LVLRKHGDAH--KLVCYFTNWA-FSRPGFASILPRDLDPFLCTHLEVA 57
Qy 68 FAKIDEVYKTIQVDPDQDNHNSWEKRGYERFNRLKKNPELTMTLSLGGWYEGSEKYS 127
Db 58 FASMSNNQ--IVPKDPLD-----EKILYFENFKLERNRGLKLLSIGWNFGIVRFT 108
Qy 128 DMAANPTYROOFTQSVLDFLOEYKFDGLDMEYPGSRGLGNPKIDKONVIALVRELKDAF 187
Db 109 KMLSTFNRERFVSSVIALRTHGFDGLDLFFLYPGLR-GSPARDRTWTFVLEELLQAF 167

DR SMART; SMO0636; Glyco_18; 1.
DR PROSITE; PS01095; CHITINASE_18; FALSE NEG.
KW Glycoprotein; Fertilization; Repeat; Signal.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 721 OVIDUCT-SPECIFIC GLYCOPROTEIN.
FT DOMAIN 486 632 21 X 7 AA TANDEM REPEATS OF S-K-T-T-
[TAP]-G-[IV].
FT CARBOHYD 402 402 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 442 442 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 469 469 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 721 AA; 78807 MW; 37246C8F01665652 CRC64;

Query Match 21.9%; Score 680; DB 1; Length 721;
Best Local Similarity 33.7%; Pred. No. 3.6e-30;
Matches 175; Conservative 79; Mismatches 184; Indels 82; Gaps 16;

QY 34 RIVYVGTWVSVHKVDPIYI--EDIDPFKTHLMVGFADIKVYKTIQVDFPDQDNHNS 91
DB 23 KLVCYFTNWA-HSRPGASIMHDLDFLCTHLIFAFASMSNNQI---VAKLQDENVL- 77
QY 92 WEKRGYERFNNLRKLNPELTWISLGGWYEGSEKYSMAANPTYRQOFTQSVLDLQEVK 151
DB 78 ----YPEFNKLRNRELKTLISIGWNGFTSRFTALTSLANREKPIDSVISFLRIGH 132
QY 152 FDGLDLWDYFSGRLGNPKIDQNYLALVRELKDAPEPHG-----YLLTAASVPGDK 204
DB 133 FDGLDLFFLYPLGLR-GSPPHDRWNFLLEELQFAPAREALTOHPRLLSAAVSGIPSI 191
QY 205 IDRAYDIKELNKLFDWMVMTVDYHGGWENFYGHNAPLYKRPDETDELHTYENVNTWHY 264
DB 192 IHTSYDALLGRLDQFINVLSYDLHGSWEKFTGHNSPLFSLPESDK-----SSAYAMNY 245
QY 265 YLNNGATRDKLVMGVFPFYGRAMSIDRSKLKLGDPAGKMSPPGFSGREGVLSYELCQL 324
DB 246 WRKLGTPADKLINGFTYGRNFVLLKESKNGIQTASMGSPASPKYTKQAGFLAYEVCSF 305
QY 325 FQKEWHIYDYNNAPYNDKIKWGYDDLASICKLAFLKELGVSGVMVMSLENDDFK 384
DB 306 VQRAKKH--WIDYQYVYAFKGEWLGDDTISFSYKAMYVREHFGAGVWTLWDMDVR 363
QY 385 G-HCG-PKNPLNKVHNNWINGEKSPFGLPSTTTPP----- 422
DB 364 GTFCGNGPFLPHILNELLVQTESN-----TLPQFWFTSSVNASGPGSENTAL 413
QY 423 ---TTPTPTPTPTPTPTPTTP-----TTTPS--PTTPTPTPTPTPTPTPTPTPT 469
DB 414 TEVLITDTIKILPPGGEAMTTEVHRRYENNTVPDGSVTPCGTASPRKHAVTPENTWA 473
QY 470 PTPTPT-----APTSTPTPTPT---EHTSETPKYTYV 500
DB 474 AEAKTWSTLDFSKITTYGSKITTYGSKITTYGSKITTYGV 513

RESULT 13
OGP_HUMAN
ID OGP_HUMAN STANDARD; PRT; 578 AA.
AC Q12889; Q15841;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Oviduct-specific glycoprotein precursor (Oviductal glycoprotein)
DE (Oviductin) (Estrogen-dependent oviduct protein) (Mucin 9).
GN OVGPI OR OGP OR MUC9.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Oviduct;
RX MEDLINE=95119256; PubMed=7819450;
RA Arias E.B., Verhage H.G., Jaffe R.C.;
RT "Complementary deoxyribonucleic acid cloning and molecular

RT characterization of an estrogen-dependent human oviductal
RT glycoprotein.";
RL Biol. Reprod. 51:685-694(1994).
RN [2]
RP SEQUENCE FROM N.A., AND VARIANT GLN-676.
RA Jaffe R.C.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Coville G.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
CC !- FUNCTION: Binds to oocyte zona pellucida in vivo. May play a role
CC in the fertilization process and/or early embryonic development.
CC !- SUBCELLULAR LOCATION: Secretory granules.
CC !- TISSUE SPECIFICITY: Oviduct.
CC !- SIMILARITY: Belongs to family 18 of glycosyl hydrolases.
CC
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CC or send an email to license@sib-sib.ch).
CC
CC EMBL; U09550; AAB86946.1; -
DR EMBL; U58010; AAB04126.1; -
DR EMBL; U58001; AAB04126.1; JOINED.
DR EMBL; U58002; AAB04126.1; JOINED.
DR EMBL; U58003; AAB04126.1; JOINED.
DR EMBL; U58004; AAB04126.1; JOINED.
DR EMBL; U58005; AAB04126.1; JOINED.
DR EMBL; U58006; AAB04126.1; JOINED.
DR EMBL; U58007; AAB04126.1; JOINED.
DR EMBL; U58008; AAB04126.1; JOINED.
DR EMBL; U58009; AAB04126.1; JOINED.
DR EMBL; AL390195; CAC36039.1; -
DR MIM; 603578; -
DR GO; GO:0007565; P:pregnancy; TAS.
DR InterPro; IPR001223; Glyco_hydro_18.
DR InterPro; IPR001579; Glyco_hydro_18AS.
DR Pfam; PF00704; Glyco_hydro_18; 1.
DR ProDom; PD000471; Glyco_hydro_18; 1.
DR SMART; SMO0636; Glyco_18; 1.
DR PROSITE; PS01095; CHITINASE_18; FALSE NEG.
KW Glycoprotein; Fertilization; Signal; Polymorphism.
FT SIGNAL 1 21 BY SIMILARITY.
FT CHAIN 22 678 OVIDUCT-SPECIFIC GLYCOPROTEIN.
FT CARBOHYD 402 402 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 441 441 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 580 580 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 596 596 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 648 648 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 676 676 E -> Q (in dbSNP:7825).
FT CONFLICT 477 477 M -> T (IN REF. 2).
FT CONFLICT 511 511 S -> P (IN REF. 2).
FT CONFLICT 514 514 Y -> H (IN REF. 2).
SQ SEQUENCE 678 AA; 75421 MW; 245F2CEDEC92768B CRC64;

Query Match 21.5%; Score 668; DB 1; Length 678;
Best Local Similarity 33.1%; Pred. No. 1.5e-23;
Matches 176; Conservative 91; Mismatches 192; Indels 72; Gaps 19;

QY 10 IMACIGLWNASIKEDNDYKSNPRIVCYVGTWVSVHKVDPIYI--EDIDPFKTHLMYG 67
DB 4 LLLMWGLV---LVLRHHDGAH--KLVCYFTNWA-HSRPGASIMHDLDFLCTHLIFA 57
QY 68 FAKIDVYKYTIQVDFPDQDNHNSWEKRGYERFNNLRKLNPELTWISLGGWYEGSEKYS 127
DB 58 PASMNNQI---VAKDLQD-----EKLIPFNKLRNRELKTLISIGWNGFTSRFT 108

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OM protein - protein search, using sw model

Run on: March 22, 2004, 06:39:53 ; Search time 111.679 Seconds
(without alignments)
1568.003 Million cell updates/sec

Title: US-09-662-293-18
Perfect score: 3107
Sequence: 1 MKTIVAILGIMAGIGLMNAS.....IMPCPGTIWCQKLTICGE 555

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL 25:.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3107	100.0	555	Q9U6R7	Q9U6R7 dermatophag
2	1008.5	32.5	525	Q44079	Q44079 anopheles g
3	942	30.3	431	Q818H5	Q818H5 araneus ven
4	869	28.0	1635	Q17412	Q17412 aedes aegypt
5	854.5	27.5	4498	Q9W223	Q9W223 drosophila
6	847	27.3	544	Q9GQC4	Q9GQC4 bombyx mori
7	842	27.1	2838	Q8MP05	Q8MP05 tenebrio mo
8	839	27.0	566	Q8WR52	Q8WR52 bombyx mori
9	837.5	27.0	467	Q15993	Q15993 penaeus jap
10	837.5	27.0	543	Q9GR93	Q9GR93 bombyx mori
11	837.5	27.0	543	Q9GV05	Q9GV05 bombyx mori
12	837.5	27.0	565	P90710	P90710 bombyx mori
13	837.5	27.0	535	Q9VFR3	Q9VFR3 drosophila
14	832	26.8	460	Q9W2M7	Q9W2M7 drosophila
15	831.5	26.8	467	Q8ITU3	Q8ITU3 penaeus van
16	829.5	26.7	565	Q9GPG9	Q9GPG9 bombyx mand

17	823.5	26.5	557	5	Q8MTK0	Q8mtk0 choristoneu
18	823	26.5	488	13	Q90W34	Q90w34 bufo japoni
19	814.5	26.2	552	5	Q9GV44	Q9gv44 spcdoptera
20	810	26.1	574	5	Q17411	Q17411 aedes aegypt
21	802	25.8	483	5	Q23737	Q23737 chelonus sp
22	798	25.7	572	5	Q26042	Q26042 penaeus jap
23	790	25.4	620	5	Q9Y0D4	Q9y0d4 penaeus mon
24	787	25.3	553	5	P91731	P91731 hyphantria
25	780	25.1	470	13	Q803B7	Q803b7 brachydanio
26	762.5	24.5	474	5	Q86L22	Q86l22 lutzomyia l
27	754	24.3	500	13	Q7ZV48	Q7zv48 brachydanio
28	738	23.8	466	4	Q13231	Q13231 homo sapien
29	736.5	23.7	473	11	Q99PH2	Q99ph2 mus musculu
30	734.5	23.6	472	11	Q9JLN1	Q9jln1 mus musculu
31	734.5	23.6	473	11	Q9D803	Q9d803 mus musculu
32	733	23.6	482	13	Q8AV87	Q8av87 gallus gall
33	732.5	23.6	387	4	Q9H3V8	Q9h3v8 homo sapien
34	731.5	23.5	472	6	Q9SM17	Q9sm17 bos taurus
35	723.5	23.3	688	5	Q8MS85	Q8ms85 drosophila
36	722.5	23.3	1013	5	Q960M0	Q960m0 drosophila
37	717	23.1	527	5	P91773	P91773 penaeus jap
38	716	23.0	460	5	Q8WS95	Q8ws95 glossina mo
39	710	22.9	484	5	Q9W092	Q9w092 drosophila
40	708.5	22.8	476	4	Q9BZP6	Q9bzp6 homo sapien
41	703	22.6	929	5	Q8MY79	Q8my79 haemaphysal
42	702.5	22.6	983	5	Q9VZV2	Q9vzv2 drosophila
43	691	22.2	462	5	Q9W2M6	Q9w2m6 drosophila
44	687	22.1	381	11	Q99J84	Q99j84 mus musculu
45	687	22.1	389	11	Q8BKL8	Q8bkl8 mus musculu

ALIGNMENTS

RESULT 1

Q9U6R7
ID Q9U6R7 PRELIMINARY; PRT; 555 AA.
AC Q9U6R7;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE 98kDa HDM allergen.
OS Dermatophagoides farinae (House-dust mite).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC Acariformes; Sarcotiformes; Astigmata; Psoroptidia; Analgoidea;
OC Pyroglyphidae; Dermatophagoides.
OX NCBI_TaxID=6954;
RN [1]_TaxID=6954;
RP SEQUENCE FROM N.A.
RA Weber E.R., Hunter S., Steadman K., McCall C.;
RT "Cloning and Characterization of a 98 kDa Allergen from
RT Dermatophagoides farinae";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF178772; AAC52672.1; -
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008061; F:chitin binding; IEA.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0006030; P:chitin metabolism; IEA.
DR InterPro; IPR002557; Chitin bind PexA.
DR InterPro; IPR01223; Glyco hydro 18.
DR InterPro; IPR01579; Glyco hydro 18AS.
DR Pfam; PF00704; Glyco hydro_18; 1-
DR ProDom; PD000471; Glyco_hydro_18; 1.
DR SMART; SM00494; ChtBD2; 1.
DR SMART; SM00636; Glyco 18; 1.
DR PROSITE; PS01095; CHITINASE_18; 1.
KW Glycosidase; Hydrolase.
SQ SEQUENCE 555 AA; 63238 MW; 0B4564A1A459B30B CRC64;

Query Match 100.0%; Score 3107; DB 5; Length 555;
Best Local Similarity 100.0%; Pred. No. 2.9e-186;
Matches 555; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MKTIYAILSIACIGLMNASIKRDHNDYSKNPMRIYCVGTWSTVYHKVDYPTTIEDIDPFK 60
D 1 MKTIYAILSIACIGLMNASIKRDHNDYSKNPMRIYCVGTWSTVYHKVDYPTTIEDIDPFK 60
QY 61 CTHLMYFPAKIDYKTIQVDPDPYQDDNHNWSWKRGRYERFNNLRLKNPELTMTISLGGWY 120
D 61 CTHLMYFPAKIDYKTIQVDPDPYQDDNHNWSWKRGRYERFNNLRLKNPELTMTISLGGWY 120
QY 121 EGSKYSMAANPYRQFIQSVLDLQYKFDGLDLDWEYFGSLGNPKIDKONYLALV 180
D 121 EGSKYSMAANPYRQFIQSVLDLQYKFDGLDLDWEYFGSLGNPKIDKONYLALV 180
QY 181 RELKDAPEPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYGWENFYGHNA 240
D 181 RELKDAPEPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYGWENFYGHNA 240
QY 241 PLYKRPDDELHYFNNVMTYLLNGATRDKLVMGVPPFYGRAMSIEDRSKLKGDPA 300
D 241 PLYKRPDDELHYFNNVMTYLLNGATRDKLVMGVPPFYGRAMSIEDRSKLKGDPA 300
QY 301 KGMSPPGFISGEGVLSYIELCOLFOKEEWHIOYDEYNNAPYGYNDKIWGYDDLASISC 360
D 301 KGMSPPGFISGEGVLSYIELCOLFOKEEWHIOYDEYNNAPYGYNDKIWGYDDLASISC 360
QY 361 KLAFLKELGVSMVMSLENDDFKGGCPKNPLNKVHNMINGDEKNSFCILGPSTTP 420
D 361 KLAFLKELGVSMVMSLENDDFKGGCPKNPLNKVHNMINGDEKNSFCILGPSTTP 420
QY 421 TPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTT 480
D 421 TPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTT 480
QY 481 TSPSTTHTSETPKYTYVDGHLIKCYKEGDIHPHNTIHKYLVCBFVNGGWVHIMPCP 540
D 481 TSPSTTHTSETPKYTYVDGHLIKCYKEGDIHPHNTIHKYLVCBFVNGGWVHIMPCP 540
QY 541 PGTIWCQKLCIG 555
D 541 PGTIWCQKLCIG 555

RESULT 2
O44079 PRELIMINARY; PRT; 525 AA.
ID O44079
AC O44079;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Chitinase.
GN AGCHI-1.
OS Anopheles gambiae (African malaria mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX NCBI_TaxID=7165;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Gut;
RX MEDLINE=98030563; PubMed=9360958;
RA Shen Z, Jacobs-Lorena M.;
RT "Characterization of a novel gut-specific chitinase gene from the
RT human malaria vector Anopheles gambiae."
RL J. Biol. Chem. 272:28895-28900(1997).
DR EMBL; AF008575; AAB87764.1; -.
DR PIR; T4445; T4445.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008061; F:chitin binding; IEA.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0006030; P:chitin metabolism; IEA.
DR InterPro; IPR002557; Chitin bind PerA.
DR InterPro; IPR001223; Glyco_hydro_18.
DR InterPro; IPR001579; Glyco_hydro_18AS.
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DR Pfam; PF01507; CBM_14; 1.
DR Pfam; PF00704; Glyco_hydro_18; 1.
DR ProDom; PD000471; Glyco_hydro_18; 1.
DR SMART; SM00494; ChtBD2; 1.
DR SMART; SM00636; Glyco_18; 1.
DR PROSITE; PS01095; CHITINASE_18; 1.
KW Glycosidase; Hydrolase.
SQ SEQUENCE 525 AA; 57211 MW; 3234360BEFF36165 CRC64;

Query Match 32.5%; Score 1008.5; DB 5; Length 525;
Best Local Similarity 38.4%; Pred. No. 4e-55;
Matches 211; Conservative 93; Mismatches 187; Indels 59; Gaps 13;

QY 8 LSIMACIGLMNASIKRDHNDYSKNPMRIYCVGTWSTVYHKVDYPTTIEDIDPFKCTHLM 65
D 5 VGVILVAVAAFAEPEHKAASGKVKVVCVGTWAVRPGNGRYDIEHIDPSLCTHLM 64
QY 66 YGFAKIDYKTIQVDPDPYQDDNHNWSWKRGRYERFNNLRLKNPELTMTISLGGWEGSEK 125
D 65 YGFFGNE-DATVRIIDPYLDLEN-WGRGHIKREVLGNVPGGLKTLAAIGMNEGRK 122
QY 126 YSDMAANPYRQFIQSVLDLQYKFDGLDLDWEYFGSLGNPKIDKONYLALVRELKD 185
D 123 FSMAASGELRKRFISDCVAFQCRHGFQDLDWEYPAQRDGNPLIDRDNHAQLVEEMRE 182
QY 186 APEPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYGWENFYGHNAPLYKR 245
D 183 EFDHYGLLLTAAVASVERPSAGSYDI PRISKSFHLNVMTYDMHGANDSYCCGINAPLYRG 242
QY 246 PDDELHYFNNVMTYLLNGATRDKLVMGVPPFYGRAMSIEDRSKLKGDPAKGMSP 305
D 243 SADTTDLRLQILNVNASIHFWLAQGGCTGRKVLGIPLYGRNFTLASAANTQIGAPTVGGT 302
QY 306 PGFISGEGVLSYIELCOLFOKEEWHIOYDEYNNAPYGYNDKIWGYDDLASISCLAPL 365
D 303 VGRYTRPGVNGYNEFCEKLAATEAWDLRSEBQQVYAVRNNQWGYDDLSVQLKVKYL 362
QY 366 KELGVSMVMSLENDDFKGGHC-GPKNPLNKVHNMINGDEKNSFECILGPSTTPTPT 424
D 363 LDQGLGMVMSLETDPLGVCGGRYPLMHHSIRSLVNGT-----PSTTWPSPV 413
QY 425 TPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTT 484
D 414 APTT-----STVAPGTTTTTPTGANPTQPTT--SDAPNHTTTTTEGNEGPTTTPSG 466
QY 485 TTEHTSETPKYTYVDGHLIKCY--KEGDIHPHNTIHKYLVC-----EFVNGGWVH 535
D 467 -----DG---FCAGGRYGVPHPTNCARYICLTADTVYEFT----- 500
QY 536 IMPCPGTIW 545
D 501 ---CPGTIF 507
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RESULT 3

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Q81SH5 PRELIMINARY; PRT; 431 AA.
ID Q81SH5
AC Q81SH5;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Chitinase.
OS Araneus ventricosus.
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
OC Araneomorphae; Entelegynae; Araneioidea; Araneidae; Araneus.
OX NCBI_TaxID=182803;
RN [1]
RP SEQUENCE FROM N.A.
RA Han J.H., Kim S.R., Sohn H.D., Jin B.R.;
RT "Molecular cloning of a cDNA encoding the chitinase from the spider,
RT Araneus ventricosus."
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY120879; AAN39100.1; -.
```

DR	GO; GO:0016787; F:hydrolase activity; IEA.	DR	GO; GO:0005576; C:extracellular; IEA.
DR	GO; GO:0005975; P:carbohydrate metabolism; IEA.	DR	GO; GO:0008061; F:chitin binding; IEA.
DR	InterPro; IPR001223; Glyco_hydro_18.	DR	GO; GO:000843; F:endochitinase activity; IEA.
DR	Pfam; PF00704; Glyco_hydro_18; 1.	DR	GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR	ProDom; PD000471; Glyco_hydro_18; 1.	DR	GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR	SMART; SM00636; Glyco_18; 1.	DR	GO; GO:0006032; P:chitin catabolism; IEA.
DR	PROSITE; PS01095; CHITINASE_18; 1.	DR	InterPro; IPR002557; Chitin_bind_Pera.
SQ	SEQUENCE 431 AA; 47238 MW; 929439397B9BC23 CRC64;	DR	InterPro; IPR001223; Glyco_hydro_18.
Query Match 30.3%; Score 942; DB 5; Length 431;			
Best Local Similarity 43.8%; Pred. No. 4.6e-51;			
Matches 185; Conservative 78; Mismatches 135; Indels 26; Gaps 9;			
QY	12 ACIGLM--NASIKRDHNSKEMRIVCVGTWSVYHKVD-PYTIEDIDPFKCHLMYGF 68	QY	21 IKRDHNSKNPM-----RIVCVGTWSVYHKVD-PYTIEDIDPFKCHLMYFPAKIDE 73
DB	6 ACILLLLVAVSAQSRDRNQKKYKVCVLGSWANYRGGEKFLIEHIDPFLCTHYVGF 65	DB	650 INKETSNDENAIESDVKVVCYFTNWAQVQGNKGLPEDIDADLCTHYVGFVLD 709
QY	69 AKIDEYKTIQVDPYODDNHNSWKRGERFNNLRKLNPELTMTISLGGWEGSKYSD 128	QY	74 YKTIQVDPYQDDNNHNSW---EKRYERFNNLRKLNPELTMTISLGGWEGSKYSD 129
DB	66 AKLSNQ--IAVDPYLDLKEN-WGLGAFORFNNLRKLNPELTMTISLGGWEGSKYSA 122	DB	710 DRLVTK-----PHDSWADIDNRFYERVVEYKKKKKVT--VAIGWNSAGSKYSL 759
QY	129 MAANPTVROFIOGVLDLQYKFDGLDWEYVPSGLNPKIDKQNYLALVRELKDAFE 188	QY	130 RANPTVROFIOGVLDLQYKFDGLDWEYVPSGLNPKIDKQNYLALVRELKDAFE 185
DB	123 MAADPNARATFKVSDVDFCLKYDFDGLDMDWEYPANR-GGAADHKQNFVTLKELKEAFA 181	DB	760 VSAARAKQFADVVAFIEKYFGDGLDWEYVPCWQVDCKKGFSDKEGEFASLVVLSQ 819
QY	189 PHGVLLTAAPSPGKDKIDRAYDIKELNKLFDMMVNTYDVGWENFYGHNAPLYKRPDE 248	QY	186 AFEPHGVLTLTAAPSPGKDKIDRAYDIKELNKLFDMMVNTYDVGWENFYGHNAPLYK 245
DB	182 PHGLLSAAVSAQSNITIDAYDIPGVAKYLDFFINWAYDLGSEWKTAGHNAPLYRPE 241	DB	820 AFKPKGLLSSAVSPSKVDEGYDVTLSYDMVIAVAYDYGQWKKTKGHVAPWYEH 879
QY	249 TDELHTYFNVNYTMHYLLNNGATDKLVMGVPPFYGRAWSIEDRSKLGDPAGKMSPPGF 308	QY	246 PDETDELHTYFNVNYTMHYLLNNGATDKLVMGVPPFYGRAWSIEDRSKLGDPAGKMS 305
DB	242 -PESDKILNDVAINWIKNGTPKNKVLGMGYGRSFTLANAANGLGNAITGPSAGP 300	DB	880 PDDPDKT--FWANFTIHWIEKGDPRKLVGMHPMYGQSPSLADNKEHGLNAKTYGGE 936
QY	309 ISGEGVLSYELCOLFQKEWHIQYDEYNAPYGYNDKIWGYDGLASISCKLAPLKL 368	QY	306 PGFISGEGVLSYELCOLFQKEWHIQYDEYN-APYGYNDKIWGYDGLASISCKLAP 364
DB	301 LTKPEGLMGVNEIC--SDKGWNEVFVEKAPYAYKGNQWGYSDVSKSIGIKVDYLIRE 357	DB	937 AGESTRARGFLSYEICANIRNKWTVARDKRGMPYAYKGDQWVSDQVMIRHKSEY 996
QY	369 GVSGVWWSLENDDFKHC-PRKPLNKKVHNMINGDEKNSFCILGPSTPTPTPTT 427	QY	365 LKELGVSGVWWSLENDDFKHC-PRKPLNKKVHNMINGDEKNSFCIL--GPSTPTPT 421
DB	358 GLGGMTWSLETDGFRGCGGKYPLLTTIASKLNGD-----VARPTDPDK 403	DB	997 VKAMGLGGAMIWALDDFRNLDCCEEYPLLRINRVLNRNYPGPGRCVLEKEPQREPR 1056
QY	428 TPTT 431	QY	422 PTTTPT 481
DB	404 QPTT 407	DB	1057 PTPRPTS-----TTPETTRRPTSTTSTRRTTMTTIT--TTTRPTPTPTPTPTPT 1104
RESULT 4			
QY	017412 PRELIMINARY; PRT; 1635 AA.	QY	482 PSPTTTEHTSETPKY-----TTVVDGHLIKCYKEGDIPHPHTNIIKYLVCDFVNGW 532
DB	017412; (TrEMBLrel. 05, Created)	DB	1105 PPTTPTT---NVPSYQETIANEVDFTCTDGLF-----VPHPTDCNKYICQYK--- 1150
QY	01-JAN-1998 (TrEMBLrel. 05, Last sequence update)	QY	533 WYHIMPCPPGTIW-----CQEKLT 551
DB	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)	DB	1151 -----LCPGGLYWSVDHCDWDPQSTNCRNKQT 1176
QY	Probable chitinase 2 (EC 3.2.1.14).	QY	SEQUENCE FROM N.A.
DB	CH22.	DB	MEDLINE=98324849; PubMed=9662472;
QY	Aedes aegypti (Yellow fever mosquito).	DB	de la Vega H., Specht C.A., Liu Y., Robbins P.W.;
DB	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;	DB	"Chitinases are a multi-gene family in Aedes, Anopheles and
QY	Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.	DB	Drosophila.";
DB	NCBI_TaxID=7159;	DB	Insect Mol. Biol. 7:233-239(1998).
QY	[1]	DB	-!- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF N-
DB	ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.	DB	-!- SIMILARITY: BELONGS TO CHITINASE CLASS II (FAMILY 18 OF GLYCOSYL
QY	HYDROLASES).	DB	HYDROLASES).
DB	EMBL; AF026492; AAB81850.1; -.	DB	PIR; T14075; T14075.


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DR InterPro; IPR001223; Glyco_hydro_18.
DR InterPro; IPR001579; Glyco_hydro_18AS.
DR Pfam; PF01607; CBM_14; 1.
DR Pfam; PF00704; Glyco_hydro_18; 1.
DR ProDom; PD000471; Glyco_hydro_18; 1.
DR SMART; SM00494; ChtBD2; 1.
DR SMART; SM00636; Glyco_18; 1.
DR PROSITE; PS01095; CHITINASE_18; 1.
DR Glycosidase; Hydrolase.
SQ SEQUENCE 544 AA; 61069 MW; 89872DFC1DA23753 CRC64;

Query Match 27.3%; Score 847; DB 5; Length 544;
Best Local Similarity 36.5%; Pred. No. 5.2e-45;
Matches 207; Conservative 78; Mismatches 218; Indels 64; Gaps 19;

QY 1 MKTIYAILSIMA-CIGIMNASIKRDNYSKPMRIVCVGTWSVYHK-VDPYTTIEDIDP 58
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1 MRAIFATLAVLASCAALVQCADR-----ARIVCFNSWAVRPGVGRYGIEDIPV 51
QY 59 FKCTHLMYGFADKIDYKIQVDPYQDDHNSWEKRGYERFNNLRKKNPELTTLISLGG 118
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
52 DLCTHLIYFVIGTEKSSSEVLIIDPELD-----VDKSGFRNFTSLRSKHPDKFWVAVGG 106
QY 119 WYEGSEKYSDMAANPTVYRQFIOSLDFLOEYKFDGLDLDWEYPSGR-LGNPKIDKQNYL 177
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
107 WAEGGKYSNVAQKSTRSFIRKSVDFLKKYDFDGLDLDWEYFGAADRGGFSFKDEFL 166
QY 178 ALVRELKDAF--BPHGYLLTAASPGKDKIDRAYDIKELNKLFDWMNVNTYDHGGWENF 235
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
167 YFVQELKRAFTRADRGWELTAAPLANFRLMEGYHYVELCQELDAIHVMSYDLRGWAGF 226
QY 236 YGNAPLYKRPDDELTHTYFNVNTHYVYLNNGATDKLVMGVPPYGRANWIED----- 290
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
227 ADVHSPLYKRPDP-QWAYEKLVNDGLNWEKGCPTNKLWVGPYGRSFTLSAGNNY 285
QY 291 -----RSKLKLDPAKGMSPPGFISGEEGLSVIELCQLFQKE--EWHIQVDEYNAPY 342
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
286 GLGTYNKEAGGDPAFYNTATGF-----WAYEICTVEDADGSGTWKKWDEFKCPY 338
QY 343 GYNDKIVGWYDDLASISCKLAFKELGVSQVWVWSLENDDFKGHCQPKNPLANKVHNMIN 402
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
339 AYKGTQWGVEDPRSEVIEKNNWIKKEGYLGAMTWAIDMDDFKGLCGEENFLIKLH--- 394
QY 403 GDEKNSPECILGFSST---TPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTT 459
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
395 ---KMSITYVPPARTGHAPTPEW--ARPPSTPSDPSGDPI---PTTTTIVKPTTT 445
QY 460 TTPSPPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPT 518
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
446 RTTARPT--TTTIVKPHGTTEEDFDINVRPEVEBEPPTENEVDNADV-CNSEDDYVDPKKE 502
QY 519 IHKLVCFEYVNGGWVHIMCPGQTIV 545
DB 503 CSKYWRG--VNGEGVQ--FSCQPGTIF 525

RESULT 7
ID Q8MP05 PRELIMINARY; PRT; 2838 AA.
AC Q8MP05;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Chitinase precursor (EC 3.2.1.14).
GN CHIT5.
OS Tenebrio molitor (Yellow mealworm).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
OC Tenebrionidae; Tenebrio.
OX NCBI_TaxID=7067;
RN [1]
RP SEQUENCE FROM N.A.
RA Royer V., Fraichard S., Bouhin H.;

RT "A Novel putative insect Chitinase with multiple catalytic domains :
RT hormonal regulation during metamorphosis.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ487081; CAD31740.4; -.
DR GO; GO:000576; C:extracellular; IEA.
DR GO; GO:0008061; F:chitin binding; IEA.
DR GO; GO:0008843; F:endochitinase activity; IEA.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0006520; P:amino acid metabolism; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0006030; P:chitin metabolism; IEA.
DR InterPro; IPR002557; Chitin_bind_Pera.
DR InterPro; IPR001223; Glyco_hydro_18.
DR InterPro; IPR001579; Glyco_hydro_18AS.
DR InterPro; IPR000634; S/T_dehydrtase_BS.
DR Pfam; PF01607; CBM_14; 5.
DR Pfam; PF00704; Glyco_hydro_18; 5.
DR ProDom; PD000471; Glyco_hydro_18; 5.
DR SMART; SM00494; ChtBD2; 5.
DR SMART; SM00636; Glyco_18; 5.
DR PROSITE; PS01095; CHITINASE_18; 3.
DR PROSITE; PS00165; DEHYDRATASE_SER_THR; 1.
DR SIGNAL; Hydrolase; Glycosidase.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 2838 CHITINASE.
SQ SEQUENCE 2838 AA; 321407 MW; 609B3F2A8E98B9B7 CRC64;

Query Match 27.1%; Score 842; DB 5; Length 2838;
Best Local Similarity 32.2%; Pred. No. 7.8e-44;
Matches 198; Conservative 92; Mismatches 205; Indels 120; Gaps 21;

QY 31 NP---MRIVCYVGTWSVYHK-VDPYTTIEDIDPCKTHLMYGFADKIDYKIQVDPYQD 86
DB 1919 NPSEFKVVCYFTNWAYTRQGGKYLPSDDIDPDCITHIVGFVAVLQDLIKPHDTWAD 1978
QY 87 DHNSWEKRGYERFNNLRKKNPELTTLISLGGWEGS-EKYSDMAANPTVYRQFIOQSVLD 145
DB 1979 -----FDNKFYEKVTAFKAG--IKVLIAGWNDSAGDKYSLRVNPPSSRRRIAHVD 2031
QY 146 FLOEYKFDGLDWEYP-----GSRGNPKIDKONYLALVELKDAFEPHYGLTAAVSP 200
DB 2032 FIENNFPGLDLDWEYPKCWQVDCNKG-PASDKSSFAEFVKELHEAFPKGWLLSAAVSP 2090
QY 201 GKDKIDRAYDIKELNKLFDWMNVNTYDHGGWENFYGHNAPLYKRPDDELTHTYFNVNY 260
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
2091 SRRVVDAGYDPTLSRYLDIAVMCYDHGQWDKITGHVAPMYAHPDDVD---ATFNTNP 2147
QY 261 THHYVYLNNGATDKLVMGVPPYGRAWSIEDRSKLGDPKAGMSPPGFISGEEGLSVIE 320
DB 2148 TIHYWIEKGADRKDLVWGMVYSGSFLADNNQNVNAPTGGGAGBETARGFLSYTE 2207
QY 321 LCOLFQKEEWHIOYDEYVN-APYGVNDKIWGYDDLASISCKLAFKELGVSQVWVWSIE 379
DB 2208 ICTNVINKGTVVRRDRGRIGYAHLRDQWVSFDDIGMRHSEFIRANGLGGMIALD 2267
QY 380 NDDPFKGHCQ-PKNPLLNKVNHNMGDEKNSPECILGSPSTTPT--PTTPTT-PTTPTPT- 434
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
2268 LDDFENLGCSEYPLLRITNRVLRDYAKDPDKCILGKASSKPTOKPTKPTKPTKPTQ 2327
QY 435 --TPSPTPTPTPTT-SPPT-----PTTTPSPPTT----- 459
DB 2328 KPTPKPSTPPYEPFQKPSQKPSYGTSTESPEPWPDPSPCRGLFVADEKNCNQYLCNQ 2387
QY 460 -----TTTTPTPTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTT 486
DB 2388 GELQLQVCPNGLFWNRDCHDWPENTCHPDGTTTAASTTTTQTLVEVEVEVEVEPTT 2447
QY 487 -----TEHTSETPKYTYVDGHLIKYKEGDIPHTNIHKYL-----VCEFNVGNGW 533
DB 2448 AAPVGTDVTEGAYKVCYFTNW--AWTAQGD-----GKYLPODIDASLCTHNYGFA 2498
QY 534 V---HIMPCPGTIV 545
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OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN SEQUENCE FROM N.A.
RP STRAIN=Berkley;
RC MEDLINE=20196006; PubMed=10731132;
RX Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt R.G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Frankoch C., Baldwin D.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Fabios B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Gaig N.S., Gelbart W.M., Glaeser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Moberly B., Murphy L., Muzny D.M., Nelson D.L.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleeb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reiner K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195 (2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nunoo J., Pacleeb J., Paragas V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF003701; AAF54987.1; -
DR EMBL; AY061553; AAL29101.1; -
DR FlyBase; FBGN0038180; CG9307.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008061; F:chitin binding; IEA.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0006030; P:chitin metabolism; IEA.
DR InterPro; IPR002557; Chitin bind perA.
DR InterPro; IPR001223; Glyco_hydro_18.
DR InterPro; IPR001579; Glyco_hydro_18AS.
DR Pfam; PF00704; Glyco_hydro_18; 1.
DR ProDom; PD000471; Glyco_hydro_18; 1.
DR SMART; SM00494; ChcBD2; 1.
DR SMART; SM00636; Glyco_18; 1.
DR PROSITE; PS01095; CHITINASE_18; 1.
DR GlycoSide; Hydrolase
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QY 88 NHNSWEKRGYVERFNNLKLKPELTWISLGGWEGSEKYSDMAANPYRQQTQSVDLDEL 147
DB 82 ----VDQGSFKFTQLKSNPNVKEIAVGMWAGGSKYSQMVAVRRRSPFRSIVRFRM 137
QY 148 QEYKFDGLDLDWEVPGS--RLGNPKDKQNYLALVRELKDAF--EPHYLLTAAVSPGKD 203
DB 138 KQYNDFDGLDWEVPGATDGGNGV-DKDKELFVRELRAFPDREGWEITWAVPAKF 196
QY 204 KIDRAYDIKELNKLFDMMNVTYDHYGGWENFYGHNAPLYKRPDETDLHLYFNVNTMH 263
DB 197 RLNEGYHVPCLCEALDAIHAMTYDLRGNWAGFADVHSPLYKPKHD-QYAYEKLNVNDGLA 255
QY 264 YYLANGATROKLVGVVFFYGRAMSIEDRSK-LKLG----DPAKMSPPGFISGEGVLSYI 319
DB 256 LWEEMGCPANKLVGVVFFYGRFTTSLNSKNYNNMTYINKEAGGGAGPGYTNASGFLAYY 315
QY 320 ELC-QLFKQEE-WHIQYDEVYNAKYNDKIKWGYDDLASICKLAFLKELGVSGVMVWS 377
DB 316 EICTEVNDKSGMTDWDAGMVPYTKDTQWVGYEASIQKDFIKORGAGATWTA 375
QY 378 LENDDFKGHGCPKNPLANKVH-NMINGDEKNSPECILGSPSTTTPTTTP-----TTPTTT 432
DB 376 IDMDDFHGMCGRKNGLTQILDNMKN-----YRVEPTRQTTTPEWAKXPAT 423
QY 433 PTTT-----SPTTPTT-----TPSTPTPTTPTT-----PTTPTTPTTPTTPTTPTT-- 473
DB 424 PPNDEGANVAPTSTTKRKPCKPSTSSPLSPSAPGVPVTVGSSSTPKPTTKPKPKPK 483
QY 474 TPAPTTPSTPTTTEHSETPKYTTY-----VDGLIKCYKEGDIHPH 516
DB 484 TTTTITTTTAPD---EKSTEEPEVYVDPVEPTDPEQPMGPQDPDNEIDCTNRDFVPHP 540
QY 517 TNIHKYLVCEVNGVGVVHNP-----CPPGT 543
DB 541 -NCRKYFR-----VHGKPVFECKEGT 562

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AC QW2M7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE CG9357 protein.
GN CG9357.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
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RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
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RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195 (2000).
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RC STRAIN=Berkley;
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RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF003701; AAF54987.1; -
DR EMBL; AY061553; AAL29101.1; -
DR FlyBase; FBGN0038180; CG9307.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008061; F:chitin binding; IEA.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0006030; P:chitin metabolism; IEA.
DR InterPro; IPR002557; Chitin bind perA.
DR InterPro; IPR001223; Glyco_hydro_18.
DR InterPro; IPR001579; Glyco_hydro_18AS.
DR Pfam; PF00704; Glyco_hydro_18; 1.
DR ProDom; PD000471; Glyco_hydro_18; 1.
DR SMART; SM00494; ChcBD2; 1.
DR SMART; SM00636; Glyco_18; 1.
DR PROSITE; PS01095; CHITINASE_18; 1.
DR GlycoSide; Hydrolase
SQ SEQUENCE 595 AA; 67050 MW; 8DC8469D3F732593 CRC64;

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RA Borkova D., Botchan M.R., Bouck J., Brockstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
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RA De Pablos B., Delcher A., Deng Z., Mays A.D., Dew I.J., Dietz S.M.,
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RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
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RA Glodek A., Gong F., Corral J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
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RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarri C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacieb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
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RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RA "The genome sequence of *Drosophila melanogaster*.";
RL Science 287:2185-2195 (2000).
DR EMBL; AE003452; AAF46663.1; --
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DR GO; GO:0005576; C:extracellular; IEA.
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DR GO; GO:0006457; P:protein folding; IEA.
DR InterPro; IPR002557; Chitin bind PerA.
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Matches 183; Conservative 87; Mismatches 175; Indels 98; Gaps 11;

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DB 1 NAASSAAGNS-SKN---VVCQGWSVTRPGLGKFGMEDIDPFCTHLYAFGLIEE-T 55

QY 76 YTIQVFDYQDNNHNSWEKRGYERFNNLRKNPELTMTISLGWYEGSEKYSDMAANPTY 135
DB 56 GQLRVIDAYLDLEENS-GEGNIKSFNALKKNPVLKTLVAVGWNEGSKRFSLVARDPSK 114

QY 136 RQQTQSVLDFLOEYKFGDLDDWEYPGSRGNPKIKQNYALVRELKDAFEPHGYLLT 195
DB 115 REKFVDDVVRFLQRHFGDLDDWEYPGSRHSLDNEGRSNITTFKELKEGLEPFGFILS 174

QY 196 AAVSPGKDKIDRAYDIKELNKLFDWMYNTYDHGWNFYGHNAPLY---KRPDETEL 252
DB 175 AAVGSAQFSAEISYDIPAMVPYLDLTINWAYDLHGFWDQVGINAPLYAAEKDSSGR 234

QY 253 HYFVNVNTMYVYLNNGATRDKLGVGPPYGRAWSIEDRSKLKLGDPKAGMSPPGFISGE 312

DB 235 QQQLNDVAVKYLKAGAPAEKILGVFFYGRSFTLTATAGNOPGAPHIGKAGNYSRE 294
QY 313 EGVLSYTELCOLFOKEWHIQDEYVNPAGYNDKIWVGYYDDLASISCKLAFKELGVSG 372
DB 295 PGVLGYNELCEMREBEWTQWEATQVFPAYRQWGVYEDPRLSKAKQAYVNDHLGG 354
QY 373 VVWVSLNDDFKGCGPK-NPLNKNVHNMINGDEKSNFECILGPSTTPTPTPTPTTT 431
DB 355 IMVWSLESDDFRGTCGQQPYELLHEINRVLFGG-----NTPSGLTTSNR 399
QY 432 TPTTPT 491
DB 388 -----NTPSGLTTSNR 399
QY 492 ETPK--YTTYVDGHLIKCYKEGDIHPHTNIHKLVCFVNGVWVHIMCPGPIWCOEK 549
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QY 550 LTC 552
DB 450 KSC 452

RESULT 15
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DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Chitinase.
OS Penaeus vannamei (Penaeid shrimp) (European white shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
OC Penaeidae; Litopenaeus.
OX NCBI_TaxID=6689;
RN [1]
RP SEQUENCE FROM N.A.
RA Chang R.C.;
RT "Cloning and characterization of a cDNA encoding a chitinase from
RT hepatopancreas of the Penaeus vanamei (Crustacea, Decapoda).";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF315689; AAN74647.1; --
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008061; F:chitin binding; IEA.
DR GO; GO:0016787; P:hydrolase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0006030; P:chitin metabolism; IEA.
DR InterPro; IPR002557; Chitin bind PerA.
DR InterPro; IPR001223; Glyco hydro 18.
DR InterPro; IPR001579; Glyco_hydro_18AS.
DR Pfam; PF01607; CBM_14; 1.
DR Pfam; PF00704; Glyco hydro 18; 1.
DR ProDom; PD000471; Glyco_hydro_18; 1.
DR SMART; SM00494; ChtBD2; 1.
DR SMART; SM00636; Glyco 18; 1.
DR PROSITE; PS01095; CHITINASE_18; 1.
DR PROSITE; PS00453; FKBP PPIASE_1; 1.
SQ SEQUENCE 467 AA; 51958 MW; 734A830C6F47F4CD CRC64;

Query Match 26.8%; Score 831.5; DB 5; Length 467;
Best Local Similarity 34.2%; Pred. No. 4.1e-44;
Matches 180; Conservative 87; Mismatches 174; Indels 85; Gaps 14;

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QY 92 WEKRGYERFNNLRKNPELTMTISLGWYEGSEKYSDMAANPTYRQQTQSVLDFLOEYK 151
DB 59 --KCAIDRFTALQKQANLKAIIAVGWNEGSKFYKWAADPYLRNRFITSSLELKKHG 116

QY 152 FDGLDDWEYPGSRGNPKIKQNYALVRELKDAFEPHGYLLTAAVSPGKDKIDRAYDI 211

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 22, 2004, 06:59:34 ; Search time 4.09116 Seconds
(without alignments)
1265.926 Million cell updates/sec

Title: US-09-662-293-13
Perfect score: 105
Sequence: 1 DPAKGMPPGFIVGEEGVLS 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1049977 seqs, 258955339 residues

Total number of hits satisfying chosen parameters: 1049977

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	101	96.2	509	14	US-10-218-743-35
5	101	96.2	509	14	US-10-218-743-38
6	99	94.3	536	14	US-10-218-743-21
7	99	94.3	555	14	US-10-218-743-15
8	99	94.3	555	14	US-10-218-743-18
9	50	47.6	143	12	US-10-424-599-238601
10	49	46.7	169	12	US-10-424-599-181344
11	48	45.7	57	9	US-09-925-302-483
12	48	45.7	350	13	US-10-067-615-6
13	48	45.7	350	13	US-10-076-754-6
14	48	45.7	350	13	US-10-076-773-6
15	48	45.7	411	8	US-08-916-625B-2

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16 48 45.7 411 9 US-09-828-739-2 Sequence 2, Appli
17 48 45.7 411 9 US-09-757-421-4 Sequence 4, Appli
18 48 45.7 411 9 US-09-874-138-2 Sequence 2, Appli
19 48 45.7 411 9 US-09-887-879-11 Sequence 11, Appli
20 48 45.7 411 9 US-09-811-088-6 Sequence 6, Appli
21 48 45.7 411 9 US-09-992-964-11 Sequence 11, Appli
22 48 45.7 411 12 US-10-211-462-67 Sequence 67, Appli
23 48 45.7 411 13 US-10-039-785-3 Sequence 3, Appli
24 48 45.7 411 13 US-10-005-842-2 Sequence 2, Appli
25 48 45.7 411 13 US-10-067-615-2 Sequence 2, Appli
26 48 45.7 411 13 US-10-052-798-1 Sequence 1, Appli
27 48 45.7 411 13 US-10-076-754-2 Sequence 2, Appli
28 48 45.7 411 13 US-10-076-773-2 Sequence 2, Appli
29 48 45.7 411 14 US-10-207-655-194 Sequence 194, App
30 48 45.7 411 14 US-10-314-410-6 Sequence 6, Appli
31 48 45.7 411 14 US-10-242-383-11 Sequence 11, Appli
32 48 45.7 411 14 US-10-288-917-1 Sequence 1, Appli
33 48 45.7 411 14 US-10-322-673-3 Sequence 3, Appli
34 48 45.7 411 14 US-10-139-785-3 Sequence 3, Appli
35 48 45.7 411 15 US-10-292-486-3 Sequence 3, Appli
36 48 45.7 411 15 US-10-333-712-4 Sequence 4, Appli
37 48 45.7 411 15 US-10-423-448-1 Sequence 1, Appli
38 48 45.7 440 9 US-09-757-421-2 Sequence 2, Appli
39 48 45.7 440 9 US-09-811-088-4 Sequence 4, Appli
40 48 45.7 440 14 US-10-314-410-4 Sequence 4, Appli
41 48 45.7 440 15 US-10-333-712-3 Sequence 3, Appli
42 46 43.8 34 12 US-10-424-599-169740 Sequence 169740,
43 46 43.8 135 12 US-10-424-599-267787 Sequence 267787,
44 45 42.9 123 12 US-10-425-114-57295 Sequence 57295, A
45 45 42.9 303 9 US-09-738-626-6409 Sequence 6409, Ap

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ALIGNMENTS

RESULT 1

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US-10-218-743-4
; Sequence 4, Application US/10218743
; Publication No. US20030096779A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; FILE REFERENCE: AL-2-C3
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/09/292,225
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: 60/098,909
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/085,295
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/098,565
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: 09/062,013
; PRIOR FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-10-218-743-4

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Query Match 100.0%; Score 105; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.6e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DPAKGMPPGFIVGEEGVLS 20

Db 1 DPAKGMPPGFIVGEEGVLS 20

Query Match 96.2%; Score 101; DB 14; Length 490;
 Best Local Similarity 95.0%; Pred. No. 9.4e-07;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DPAKGMSPPGFIVGEGVLS 20
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 Db 279 DPAKGMSPPGFITGEGVLS 298
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RESULT 4
 US-10-218-743-35
 ; Sequence 35, Application US/10218743
 ; Publication No. US20030096779A1
 ; GENERAL INFORMATION:
 ; APPLICANT: McCall, Catherine A.
 ; APPLICANT: Hunter, Shirley Wu
 ; APPLICANT: Weber, Eric R.
 ; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
 ; TITLE OF INVENTION: AND USES THEREOF
 ; FILE REFERENCE: AL-2-C3
 ; CURRENT APPLICATION NUMBER: US/10/218,743
 ; CURRENT FILING DATE: 2002-08-13
 ; PRIOR APPLICATION NUMBER: US/09/292,225
 ; PRIOR FILING DATE: 1999-04-15
 ; PRIOR APPLICATION NUMBER: 60/098,909
 ; PRIOR FILING DATE: 1998-09-02
 ; PRIOR APPLICATION NUMBER: 60/085,295
 ; PRIOR FILING DATE: 1998-05-13
 ; PRIOR APPLICATION NUMBER: 60/098,565
 ; PRIOR FILING DATE: 1998-04-17
 ; PRIOR APPLICATION NUMBER: 09/062,013
 ; PRIOR FILING DATE: 1998-04-17
 ; NUMBER OF SEQ ID NOS: 49
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO 35
 ; LENGTH: 509
 ; TYPE: PRT
 ; ORGANISM: Dermatophagoides farinae
 US-10-218-743-35

Query Match 96.2%; Score 101; DB 14; Length 509;
 Best Local Similarity 95.0%; Pred. No. 9.8e-07;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DPAKGMSPPGFIVGEGVLS 20
 |||||
 Db 298 DPAKGMSPPGFITGEGVLS 317
 |||||

RESULT 5
 US-10-218-743-38
 ; Sequence 38, Application US/10218743
 ; Publication No. US20030096779A1
 ; GENERAL INFORMATION:
 ; APPLICANT: McCall, Catherine A.
 ; APPLICANT: Hunter, Shirley Wu
 ; APPLICANT: Weber, Eric R.
 ; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
 ; TITLE OF INVENTION: AND USES THEREOF
 ; FILE REFERENCE: AL-2-C3
 ; CURRENT APPLICATION NUMBER: US/10/218,743
 ; CURRENT FILING DATE: 2002-08-13
 ; PRIOR APPLICATION NUMBER: US/09/292,225
 ; PRIOR FILING DATE: 1999-04-15
 ; PRIOR APPLICATION NUMBER: 60/098,909
 ; PRIOR FILING DATE: 1998-09-02
 ; PRIOR APPLICATION NUMBER: 60/085,295
 ; PRIOR FILING DATE: 1998-05-13
 ; PRIOR APPLICATION NUMBER: 60/098,565
 ; PRIOR FILING DATE: 1998-04-17
 ; PRIOR APPLICATION NUMBER: 09/062,013
 ; PRIOR FILING DATE: 1998-04-17
 ; NUMBER OF SEQ ID NOS: 49
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO 41
 ; LENGTH: 490
 ; TYPE: PRT
 ; ORGANISM: Dermatophagoides farinae
 US-10-218-743-41

US-10-218-743-13
 ; Sequence 13, Application US/10218743
 ; Publication No. US20030096779A1
 ; GENERAL INFORMATION:
 ; APPLICANT: McCall, Catherine A.
 ; APPLICANT: Hunter, Shirley Wu
 ; APPLICANT: Weber, Eric R.
 ; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
 ; TITLE OF INVENTION: AND USES THEREOF
 ; FILE REFERENCE: AL-2-C3
 ; CURRENT APPLICATION NUMBER: US/10/218,743
 ; CURRENT FILING DATE: 2002-08-13
 ; PRIOR APPLICATION NUMBER: US/09/292,225
 ; PRIOR FILING DATE: 1999-04-15
 ; PRIOR APPLICATION NUMBER: 60/098,909
 ; PRIOR FILING DATE: 1998-09-02
 ; PRIOR APPLICATION NUMBER: 60/085,295
 ; PRIOR FILING DATE: 1998-05-13
 ; PRIOR APPLICATION NUMBER: 60/098,565
 ; PRIOR FILING DATE: 1998-04-17
 ; PRIOR APPLICATION NUMBER: 09/062,013
 ; PRIOR FILING DATE: 1998-04-17
 ; NUMBER OF SEQ ID NOS: 49
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO 13
 ; LENGTH: 20
 ; TYPE: PRT
 ; ORGANISM: Dermatophagoides farinae
 US-10-218-743-13

Query Match 100.0%; Score 105; DB 14; Length 20;
 Best Local Similarity 100.0%; Pred. No. 7.6e-09;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPAKGMSPPGFIVGEGVLS 20
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 Db 1 DPAKGMSPPGFIVGEGVLS 20
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RESULT 3
 US-10-218-743-41
 ; Sequence 41, Application US/10218743
 ; Publication No. US20030096779A1
 ; GENERAL INFORMATION:
 ; APPLICANT: McCall, Catherine A.
 ; APPLICANT: Hunter, Shirley Wu
 ; APPLICANT: Weber, Eric R.
 ; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
 ; TITLE OF INVENTION: AND USES THEREOF
 ; FILE REFERENCE: AL-2-C3
 ; CURRENT APPLICATION NUMBER: US/10/218,743
 ; CURRENT FILING DATE: 2002-08-13
 ; PRIOR APPLICATION NUMBER: US/09/292,225
 ; PRIOR FILING DATE: 1999-04-15
 ; PRIOR APPLICATION NUMBER: 60/098,909
 ; PRIOR FILING DATE: 1998-09-02
 ; PRIOR APPLICATION NUMBER: 60/085,295
 ; PRIOR FILING DATE: 1998-05-13
 ; PRIOR APPLICATION NUMBER: 60/098,565
 ; PRIOR FILING DATE: 1998-04-17
 ; PRIOR APPLICATION NUMBER: 09/062,013
 ; PRIOR FILING DATE: 1998-04-17
 ; NUMBER OF SEQ ID NOS: 49
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO 41
 ; LENGTH: 490
 ; TYPE: PRT
 ; ORGANISM: Dermatophagoides farinae
 US-10-218-743-41

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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 38
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-10-218-743-38

Query Match          96.2%; Score 101; DB 14; Length 509;
Best Local Similarity 95.0%; Pred. No. 9.8e-07;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DPAKGMSPPGFIVGEEGVL 20
Db 298 DPAKGMSPPGFIVGEEGVL 317

RESULT 6
US-10-218-743-21
; Sequence 21, Application US/10218743
; Publication No. US20030096779A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/10/218,743
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/09/292,225
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: 60/098,909
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/085,295
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/098,565
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: 09/062,013
; PRIOR FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 536
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-10-218-743-21

Query Match          94.3%; Score 92; DB 14; Length 536;
Best Local Similarity 95.0%; Pred. No. 2.1e-06;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DPAKGMSPPGFIVGEEGVL 20
Db 279 DPAKGMSPPGFIVGEEGVL 298

RESULT 7
US-10-218-743-15
; Sequence 15, Application US/10218743
; Publication No. US20030096779A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/10/218,743
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/09/292,225
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/098,909
; PRIOR FILING DATE: 1998-09-02
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; PRIOR APPLICATION NUMBER: 60/085,295
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/098,565
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: 09/062,013
; PRIOR FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 555
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-10-218-743-15

Query Match          94.3%; Score 99; DB 14; Length 555;
Best Local Similarity 95.0%; Pred. No. 2.1e-06;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DPAKGMSPPGFIVGEEGVL 20
Db 298 DPAKGMSPPGFIVGEEGVL 317

RESULT 8
US-10-218-743-18
; Sequence 18, Application US/10218743
; Publication No. US20030096779A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/10/218,743
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/09/292,225
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: 60/098,909
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/085,295
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/098,565
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: 09/062,013
; PRIOR FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 555
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-10-218-743-18

Query Match          94.3%; Score 99; DB 14; Length 555;
Best Local Similarity 95.0%; Pred. No. 2.1e-06;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DPAKGMSPPGFIVGEEGVL 20
Db 298 DPAKGMSPPGFIVGEEGVL 317

RESULT 9
US-10-424-599-238601
; Sequence 238601, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
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; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 238601
; LENGTH: 143
; TYPES: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_57482C.1.pep
US-10-424-599-238601

Query Match 47.6%; Score 50; DB 12; Length 143;
Best Local Similarity 61.1%; Pred. No. 11;
Matches 11; Conservative 1; Mismatches 4; Indels 2; Gaps 1;

QY 2 PAKGMSPPGF--IVGEEG 17
Db 121 PNKGSDPPKFFNVGEEG 138

RESULT 10
US-10-424-599-181344
; Sequence 181344, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei

; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 181344
; LENGTH: 69
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_134769C.1.pep
US-10-424-599-181344

Query Match 46.7%; Score 49; DB 12; Length 69;
Best Local Similarity 72.7%; Pred. No. 6.8;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 PAKGMSPPGFI 12
Db 31 PKEGVSPPGFI 41

RESULT 11
US-09-925-302-483
; Sequence 483, Application US/09925302
; Patent No. US20020044941A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 483
; LENGTH: 57
; TYPE: PRT

; ORGANISM: Homo sapiens
US-09-925-302-483

Query Match 45.7%; Score 48; DB 9; Length 57;
Best Local Similarity 57.1%; Pred. No. 7.8;
Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 6 MSPPGFIVGEEV 19
Db 9 LSPGFWLGVGIL 22

RESULT 12
US-10-067-615-6
; Sequence 6, Application US/10067615
; Publication No. US20020115154A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: NOVEL TRAIL RECEPTORS, NUCLEIC ACIDS ENCODING SAME, AND
; FILE REFERENCE: 480140.432D1
; CURRENT APPLICATION NUMBER: US/10/067,615
; CURRENT FILING DATE: 2002-02-04
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-067-615-6

Query Match 45.7%; Score 48; DB 13; Length 350;
Best Local Similarity 43.8%; Pred. No. 55;
Matches 7; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 2 PAKGMSPPGFIVGEEG 17
Db 76 PSEGLCPFGHISEDG 91

RESULT 13
US-10-076-754-6
; Sequence 6, Application US/10076754
; Publication No. US20020161195A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: NOVEL TRAIL RECEPTORS, NUCLEIC ACIDS ENCODING SAME, AND
; FILE REFERENCE: 480140.432D3
; CURRENT APPLICATION NUMBER: US/10/076,754
; CURRENT FILING DATE: 2002-02-12
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-076-754-6

Query Match 45.7%; Score 48; DB 13; Length 350;
Best Local Similarity 43.8%; Pred. No. 55;
Matches 7; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 2 PAKGMSPPGFIVGEEG 17
Db 76 PSEGLCPFGHISEDG 91

RESULT 14
US-10-076-773-6
; Sequence 6, Application US/10076773
; Publication No. US20020161196A1
; GENERAL INFORMATION:

APPLICANT: Alnemri, Emad S.
TITLE OF INVENTION: NOVEL TRAIL RECEPTORS, NUCLEIC ACIDS ENCODING SAME, AND
METHODS OF USE THEREOF
FILE REFERENCE: 480140.432D2
CURRENT APPLICATION NUMBER: US/10/076,773
CURRENT FILING DATE: 2002-02-12
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 350
TYPE: PRT
ORGANISM: Homo sapiens
US-10-076-773-6

Query Match 45.7%; Score 48; DB 13; Length 350;
Best Local Similarity 43.8%; Pred. No. 55;
Matches 7; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 2 PAKGMSPPGFIVGEEG 17
Db 76 PSEGLCPGGHISEDG 91

RESULT 15

US-08-916-625B-2
Sequence 2, Application US/08916625B
Publication No. US20010010924A1
GENERAL INFORMATION:
APPLICANT: DEEN, KEITH C.
APPLICANT: YOUNG, PETER R.
TITLE OF INVENTION: TUMOR NECROSIS FACTOR RELATED
TITLE OF INVENTION: RECEPTOR, TR6
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: RATNER & PRESTIA
STREET: P.O. BOX 980
CITY: VALLEY FORGE
STATE: PA
COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/916,625B
FILING DATE: 22-AUG-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/853,684
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: 60/041,230
FILING DATE: 14-MARCH-1997
ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GH-50008-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0701
TELEX: 846169
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 411 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-916-625B-2

Query Match 45.7%; Score 48; DB 8; Length 411;
Best Local Similarity 43.8%; Pred. No. 65;

Matches 7; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
Qy 2 PAKGMSPPGFIVGEEG 17
Db 76 PSEGLCPGGHISEDG 91

Search completed: March 22, 2004, 07:45:49
Job time : 4.09116 secs

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OM protein - protein search, using sw model

Run on: March 22, 2004, 06:42:54 ; Search time 1.61201 Seconds
(without alignments)
640.518 Million cell updates/sec

Title: US-09-662-293-13

Perfect score: 105

Sequence: 1 DPAKGMSPPGFIVGEEGVLS 20

Scoring table: BLOSUM62

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Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

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Post-processing: Minimum Match 0%

Maximum Match 100%

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- 3: /cgm2_6/ptodata/2/iaa/6A_COMB.pep.*
- 4: /cgm2_6/ptodata/2/iaa/6B_COMB.pep.*
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- 6: /cgm2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	101	96.2	509	4	US-09-292-225-35
5	101	96.2	509	4	US-09-292-225-38
6	99	94.3	536	4	US-09-292-225-21
7	99	94.3	555	4	US-09-292-225-15
8	99	94.3	555	4	US-09-292-225-18
9	48	45.7	350	4	US-09-134-618-6
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12	48	45.7	411	4	US-09-134-618-2
13	48	45.7	411	4	US-10-039-785-3
14	48	45.7	412	4	US-09-333-593A-2
15	48	45.7	424	4	US-09-333-593A-8
16	48	45.7	440	3	US-08-883-036A-2
17	48	45.7	440	4	US-09-536-201-2
18	48	45.7	440	4	US-09-578-392-2
19	47	44.8	420	4	US-09-252-991A-24263
20	45	42.9	503	4	US-09-252-991A-30682
21	44	41.9	219	4	US-09-252-991A-20817
22	44	41.9	3224	2	US-08-705-660-34
23	44	41.9	3224	3	US-08-989-045-34
24	42	40.0	411	4	US-09-252-991A-18602
25	41.5	39.5	915	4	US-09-543-681A-5334
26	41	39.0	367	4	US-09-252-991A-16628
27	41	39.0	385	4	US-09-134-000C-4952

RESULT 1

US-09-292-225-4
; Sequence 4, Application US/09292225
; Patent No. 6455686
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/09/292,225
; CURRENT FILING DATE: 1999-04-15
; EARLIER APPLICATION NUMBER: 60/098,909
; EARLIER FILING DATE: 1998-09-02
; EARLIER APPLICATION NUMBER: 60/085,295
; EARLIER FILING DATE: 1998-05-13
; EARLIER APPLICATION NUMBER: 60/098,565
; EARLIER FILING DATE: 1998-04-17
; EARLIER APPLICATION NUMBER: 09/062,013
; EARLIER FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 4
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-09-292-225-4

Query Match 100.0%; Score 105; DB 4; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.6e-10; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPAKGMSPPGFIVGEEGVLS 20

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Db 1 DPAKGMSPPGFIVGEEGVLS 20

RESULT 2

US-09-292-225-13
; Sequence 13, Application US/09292225
; Patent No. 6455686
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/09/292,225

Sequence 21851, A
Sequence 349, App
Sequence 5516, Ap
Sequence 11591, A
Sequence 17, Appl
Sequence 5, Appl
Sequence 458, App
Sequence 17398, A
Sequence 5542, Ap
Sequence 3, Appl
Sequence 3, Appl
Sequence 5442, Ap
Sequence 6, Appl
Sequence 32847, A
Sequence 26412, A
Sequence 53, Appl
Sequence 6265, Ap
Sequence 21650, A

ALIGNMENTS

28 41 39.0 433 4 US-09-252-991A-21851

29 41 39.0 453 4 US-09-711-164-349

30 41 39.0 456 4 US-09-543-681A-5516

31 41 39.0 519 4 US-09-489-039A-11591

32 41 39.0 611 2 US-08-821-119-17

33 41 39.0 611 2 US-08-821-118-5

34 41 39.0 845 4 US-09-198-452A-458

35 41 39.0 1049 4 US-09-252-991A-17298

36 41 39.0 1596 4 US-09-328-352-5542

37 41 39.0 3165 2 US-08-459-146-3

38 41 39.0 3165 2 US-08-459-065-3

39 40.5 38.6 72 4 US-09-543-681A-5442

40 40.5 38.6 366 3 US-09-043-627-6

41 40.5 38.6 484 4 US-09-252-991A-32847

42 40.5 38.6 509 4 US-09-252-991A-26412

43 40 38.1 54 1 US-08-401-512-53

44 40 38.1 61 4 US-09-107-532A-6265

45 40 38.1 280 4 US-09-252-991A-21650

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; CURRENT FILING DATE: 1999-04-15
; EARLIER APPLICATION NUMBER: 60/098,909
; EARLIER FILING DATE: 1998-09-02
; EARLIER APPLICATION NUMBER: 60/085,295
; EARLIER FILING DATE: 1998-05-13
; EARLIER APPLICATION NUMBER: 60/098,565
; EARLIER FILING DATE: 1998-04-17
; EARLIER APPLICATION NUMBER: 09/062,013
; EARLIER FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 13
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-09-292-225-13

Query Match      100.0%; Score 105; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPAKGMSPPGFIVGEGVLS 20
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Db 1 DPAKGMSPPGFIVGEGVLS 20
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RESULT 3
US-09-292-225-41
; Sequence 41, Application US/09292225
; Patent No. 6455686
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/09/292,225
; CURRENT FILING DATE: 1999-04-15
; EARLIER APPLICATION NUMBER: 60/098,909
; EARLIER FILING DATE: 1998-09-02
; EARLIER APPLICATION NUMBER: 60/085,295
; EARLIER FILING DATE: 1998-05-13
; EARLIER APPLICATION NUMBER: 60/098,565
; EARLIER FILING DATE: 1998-04-17
; EARLIER APPLICATION NUMBER: 09/062,013
; EARLIER FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 41
; LENGTH: 490
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-09-292-225-41

Query Match      96.2%; Score 101; DB 4; Length 490;
Best Local Similarity 95.0%; Pred. No. 2.7e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DPAKGMSPPGFIVGEGVLS 20
   |||||
Db 279 DPAKGMSPPGFIVGEGVLS 298
   |||||

RESULT 4
US-09-292-225-35
; Sequence 35, Application US/09292225
; Patent No. 6455686
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/09/292,225
; CURRENT FILING DATE: 1999-04-15
; EARLIER APPLICATION NUMBER: 60/098,909
; EARLIER FILING DATE: 1998-09-02
; EARLIER APPLICATION NUMBER: 60/085,295
; EARLIER FILING DATE: 1998-05-13
; EARLIER APPLICATION NUMBER: 60/098,565
; EARLIER FILING DATE: 1998-04-17
; EARLIER APPLICATION NUMBER: 09/062,013
; EARLIER FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 41
; LENGTH: 490
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-09-292-225-35

Query Match      96.2%; Score 101; DB 4; Length 509;
Best Local Similarity 95.0%; Pred. No. 2.8e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DPAKGMSPPGFIVGEGVLS 20
   |||||
Db 298 DPAKGMSPPGFIVGEGVLS 317
   |||||

RESULT 6
US-09-292-225-21
; Sequence 21, Application US/09292225
; Patent No. 6455686
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/09/292,225
; CURRENT FILING DATE: 1999-04-15
; EARLIER APPLICATION NUMBER: 60/098,909
; EARLIER FILING DATE: 1998-09-02
; EARLIER APPLICATION NUMBER: 60/085,295
; EARLIER FILING DATE: 1998-05-13
; EARLIER APPLICATION NUMBER: 60/098,565
; EARLIER FILING DATE: 1998-04-17
; EARLIER APPLICATION NUMBER: 09/062,013
; EARLIER FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 38
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-09-292-225-38

Query Match      96.2%; Score 101; DB 4; Length 509;
Best Local Similarity 95.0%; Pred. No. 2.8e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DPAKGMSPPGFIVGEGVLS 20
   |||||
Db 298 DPAKGMSPPGFIVGEGVLS 317
   |||||

RESULT 5
US-09-292-225-38
; Sequence 38, Application US/09292225
; Patent No. 6455686
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/09/292,225
; CURRENT FILING DATE: 1999-04-15
; EARLIER APPLICATION NUMBER: 60/098,909
; EARLIER FILING DATE: 1998-09-02
; EARLIER APPLICATION NUMBER: 60/085,295
; EARLIER FILING DATE: 1998-05-13
; EARLIER APPLICATION NUMBER: 60/098,565
; EARLIER FILING DATE: 1998-04-17
; EARLIER APPLICATION NUMBER: 09/062,013
; EARLIER FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 38
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-09-292-225-38

Query Match      96.2%; Score 101; DB 4; Length 509;
Best Local Similarity 95.0%; Pred. No. 2.8e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DPAKGMSPPGFIVGEGVLS 20
   |||||
Db 298 DPAKGMSPPGFIVGEGVLS 317
   |||||

Query Match      96.2%; Score 101; DB 4; Length 509;
Best Local Similarity 95.0%; Pred. No. 2.8e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DPAKGMSPPGFIVGEGVLS 20
   |||||
Db 298 DPAKGMSPPGFIVGEGVLS 317
   |||||
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```
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/09/292,225
; CURRENT FILING DATE: 1999-04-15
; EARLIER APPLICATION NUMBER: 60/098,909
; EARLIER FILING DATE: 1998-09-02
; EARLIER APPLICATION NUMBER: 60/085,295
; EARLIER FILING DATE: 1998-05-13
; EARLIER APPLICATION NUMBER: 60/098,565
; EARLIER FILING DATE: 1998-04-17
; EARLIER APPLICATION NUMBER: 09/062,013
; EARLIER FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 536
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-09-292-225-21

Query Match          94.3%; Score 99; DB 4; Length 536;
Best Local Similarity 95.0%; Pred. No. 6.3e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DPAKGMSPGFTVIGEEGVLS 20
Db 279 DPAKGMSPGFTVIGEEGVLS 298

RESULT 7
US-09-292-225-15
; Sequence 15, Application US/09292225
; Patent No. 6455686
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/09/292,225
; CURRENT FILING DATE: 1999-04-15
; EARLIER APPLICATION NUMBER: 60/098,909
; EARLIER FILING DATE: 1998-09-02
; EARLIER APPLICATION NUMBER: 60/085,295
; EARLIER FILING DATE: 1998-05-13
; EARLIER APPLICATION NUMBER: 60/098,565
; EARLIER FILING DATE: 1998-04-17
; EARLIER APPLICATION NUMBER: 09/062,013
; EARLIER FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 555
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-09-292-225-15

Query Match          94.3%; Score 99; DB 4; Length 555;
Best Local Similarity 95.0%; Pred. No. 6.3e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DPAKGMSPGFTVIGEEGVLS 20
Db 279 DPAKGMSPGFTVIGEEGVLS 298

RESULT 8
US-09-292-225-18
; Sequence 18, Application US/09292225
; Patent No. 6455686
; GENERAL INFORMATION:
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/09/292,225
; CURRENT FILING DATE: 1999-04-15
; EARLIER APPLICATION NUMBER: 60/098,909
; EARLIER FILING DATE: 1998-09-02
; EARLIER APPLICATION NUMBER: 60/085,295
; EARLIER FILING DATE: 1998-05-13
; EARLIER APPLICATION NUMBER: 60/098,565
; EARLIER FILING DATE: 1998-04-17
; EARLIER APPLICATION NUMBER: 09/062,013
; EARLIER FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 555
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-09-292-225-15

Query Match          94.3%; Score 99; DB 4; Length 555;
Best Local Similarity 95.0%; Pred. No. 6.3e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DPAKGMSPGFTVIGEEGVLS 20
Db 298 DPAKGMSPGFTVIGEEGVLS 317

RESULT 9
US-09-134-618-6
; Sequence 6, Application US/09134618
; Patent No. 6417328
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: NOVEL TRAIL RECEPTORS, NUCLEIC ACIDS ENCODING SAME, AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 480140.432
; CURRENT APPLICATION NUMBER: US/09/134,618
; CURRENT FILING DATE: 1998-08-14
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-134-618-6

Query Match          45.7%; Score 48; DB 4; Length 350;
Best Local Similarity 43.8%; Pred. No. 6.7;
Matches 7; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 2 PAKGMSPGFTVIGEEG 17
Db 76 PSEGLCPGHHISDG 91

RESULT 10
US-09-329-633A-2
; Sequence 2, Application US/09329633A
; Patent No. 6252050
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Chuntharapai, Anan
; APPLICANT: Kim, K. Jin
; TITLE OF INVENTION: METHOD FOR MAKING MONOCLONAL ANTIBODIES AND
; CROSS-REACTIVE ANTIBODIES OBTAINABLE BY THE METHOD
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FILE REFERENCE: P1468R1 (REVISED)
CURRENT APPLICATION NUMBER: US/09/329,633A
CURRENT FILING DATE: 1999-06-10
PRIOR APPLICATION NUMBER: US 60/089,253
PRIOR FILING DATE: 1998-06-12
NUMBER OF SEQ ID NOS: 2
SEQ ID NO 2
LENGTH: 411
TYPE: PRT
ORGANISM: human
FEATURE:
NAME/KEY: xaa
LOCATION: 410
OTHER INFORMATION: xaa = leu or met
US-09-329-633A-2

Query Match          45.7%; Score 48; DB 3; Length 411;
Best Local Similarity 43.8%; Pred. No. 8;
Matches 7; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY      2 PAKGMSPPGFIVGEEG 17
Db      76 PSEGLCPGGHISEDG 91

RESULT 11
US-09-079-029-1
; Sequence 1, Application US/09079029
; Patent No. 6342369
; GENERAL INFORMATION:
; APPLICANT: Adams, Camilia W.
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Chundharapal, Anan
; APPLICANT: Kim, Kyung J.
; TITLE OF INVENTION: Apo-2 Receptor
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079,029
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1101R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 411 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-079-029-1

Query Match          45.7%; Score 48; DB 4; Length 411;
Best Local Similarity 43.8%; Pred. No. 8;
Matches 7; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY      2 PAKGMSPPGFIVGEEG 17
Db      76 PSEGLCPGGHISEDG 91

FILE REFERENCE: P1468R1 (REVISED)
CURRENT APPLICATION NUMBER: US/09/329,633A
CURRENT FILING DATE: 1999-06-10
PRIOR APPLICATION NUMBER: US 60/089,253
PRIOR FILING DATE: 1998-06-12
NUMBER OF SEQ ID NOS: 2
SEQ ID NO 2
LENGTH: 411
TYPE: PRT
ORGANISM: human
FEATURE:
NAME/KEY: xaa
LOCATION: 410
OTHER INFORMATION: xaa = leu or met
US-09-329-633A-2

Query Match          45.7%; Score 48; DB 3; Length 411;
Best Local Similarity 43.8%; Pred. No. 8;
Matches 7; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY      2 PAKGMSPPGFIVGEEG 17
Db      76 PSEGLCPGGHISEDG 91

RESULT 12
US-09-134-618-2
; Sequence 2, Application US/09134618
; Patent No. 6417328
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: NOVEL TRAIL RECEPTORS, NUCLEIC ACIDS ENCODING SAME, AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 480140.432
; CURRENT APPLICATION NUMBER: US/09/134,618
; CURRENT FILING DATE: 1998-08-14
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 411
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-134-618-2

Query Match          45.7%; Score 48; DB 4; Length 411;
Best Local Similarity 43.8%; Pred. No. 8;
Matches 7; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY      2 PAKGMSPPGFIVGEEG 17
Db      76 PSEGLCPGGHISEDG 91

RESULT 13
US-10-039-785-3
; Sequence 3, Application US/10039785
; Patent No. 6538938
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/039,785
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 411
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-039-785-3

Query Match          45.7%; Score 48; DB 4; Length 411;
Best Local Similarity 43.8%; Pred. No. 8;
Matches 7; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY      2 PAKGMSPPGFIVGEEG 17
Db      76 PSEGLCPGGHISEDG 91
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Db 76 PSEGLCPPGHHISEDG 91

RESULT 14

US-09-333-593A-2
; Sequence 2, Application US/09333593A
; Patent No. 6313269
; GENERAL INFORMATION:
; APPLICANT: DEEN, KEITH C.
; APPLICANT: YOUNG, PETER R.
; APPLICANT: MARSHALL, LISA A.
; APPLICANT: ROSHAK, AMY K.
; APPLICANT: TAN, KONG B.
; APPLICANT: TRUNEH, ALEMSEGED
; TITLE OF INVENTION: TUMOR NECROSIS FACTOR RELATED RECEPTOR,
; TITLE OF INVENTION: TR6
; FILE REFERENCE: GH-50008-2
; CURRENT APPLICATION NUMBER: US/09/333,593A
; CURRENT FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 08/916,625
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 08/853,684
; PRIOR FILING DATE: 1997-05-09
; PRIOR APPLICATION NUMBER: 60/041,230
; PRIOR FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 412
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-333-593A-2

Query Match 45.7%; Score 48; DB 4; Length 412;
Best Local Similarity 43.8%; Pred. No. 8;
Matches 7; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 2 PAKGMSPPGFIVGEG 17

Db 76 PSEGLCPPGHHISEDG 91

RESULT 15

US-09-333-593A-8
; Sequence 8, Application US/09333593A
; Patent No. 6313269
; GENERAL INFORMATION:
; APPLICANT: DEEN, KEITH C.
; APPLICANT: YOUNG, PETER R.
; APPLICANT: MARSHALL, LISA A.
; APPLICANT: ROSHAK, AMY K.
; APPLICANT: TAN, KONG B.
; APPLICANT: TRUNEH, ALEMSEGED
; TITLE OF INVENTION: TUMOR NECROSIS FACTOR RELATED RECEPTOR,
; TITLE OF INVENTION: TR6
; FILE REFERENCE: GH-50008-2
; CURRENT APPLICATION NUMBER: US/09/333,593A
; CURRENT FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 08/916,625
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 08/853,684
; PRIOR FILING DATE: 1997-05-09
; PRIOR APPLICATION NUMBER: 60/041,230
; PRIOR FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 424
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-333-593A-8

Query Match 45.7%; Score 48; DB 4; Length 424;

Best Local Similarity 43.8%; Pred. No. 8.3;
Matches 7; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 2 PAKGMSPPGFIVGEG 17

Db 76 PSEGLCPPGHHISEDG 91

Search completed: March 22, 2004, 07:03:57
Job time : 1.61201 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 22, 2004, 06:40:28 ; Search time 36.0951 Seconds
(without alignments)
1479.047 Million cell updates/sec

Title: US-09-662-293-15
Perfect score: 3107
Sequence: 1 MKTIYALISIMACIGLMNAS.....IMPCPPQTIWCQKLTICIG 555

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues
Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:.*
1: PIR1:.*
2: PIR2:.*
3: PIR3:.*
4: PIR4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1008.5	32.5	525	2 T44445	chitinase (EC 3.2.)
2	869	28.0	1635	2 T14075	chitinase (EC 3.2.)
3	838.5	27.0	554	2 A56596	chitinase (EC 3.2.)
4	802	25.8	483	2 A53918	chitinase (EC 3.2.)
5	705.5	22.7	617	2 T15408	hypothetical prote
6	685.5	22.1	537	2 S57197	oviduct-specific g
7	685	22.0	539	2 T46470	estrogen dependent
8	668	21.5	654	2 T38605	oviductal glycopro
9	662	21.3	383	2 A49562	cartilage glycopro
10	650	20.9	383	2 S51327	heparin-binding gl
11	646.5	20.8	405	2 S61551	breast-regressing
12	608	19.6	399	2 S27879	secretory protein
13	604.5	19.5	504	2 A38221	chitinase (EC 3.2.)
14	592	19.1	599	2 D83764	chitinase BH0916 [
15	561	18.1	699	2 A38368	chitinase (EC 3.2.)
16	560	18.0	1215	2 T43916	chitinase A [impor
17	483.5	14.9	831	2 T00323	chitinase [ec 3.2.
18	432.5	13.9	1484	2 T29275	hypothetical prote
19	428	13.8	869	2 T44440	chitinase (EC 3.2.)
20	427.5	13.8	849	2 D82510	chitinase VCA0027
21	424.5	13.7	2025	2 T03884	hypothetical prote
22	414.5	13.3	563	2 S60651	chitinase precursor
23	413	13.3	756	2 AB1452	chitinase B homolo
24	412	13.3	423	2 TQ1975	chitinase (EC 3.2.)
25	411.5	13.2	424	2 S68121	chitinase I precur
26	411	13.2	423	2 S51369	chitinase f fungus
27	409.5	13.2	756	2 AB1088	chitinase B homolo
28	408.5	13.1	561	2 A25030	chitinase (EC 3.2.)
29	405	13.0	546	2 F84238	chitinase [impor

RESULT 1

T44445
Chitinase (EC 3.2.1.14) [imported] - African malaria mosquito
C/Species: Anopheles gambiae (African malaria mosquito)
C/Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jan-2000
C/Accession: T44445
R/Shen, Z.; Jacobs-Lorena, M.
submitted to the EMBL Data Library, June 1997
A/Reference number: Z22771
A/Accession: T44445
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-525 <SHE>
A/Cross-references: EMBL:AF008575; PIDN:AAB87764.1
A/Experimental source: adult; gut
C/Genetics:
A/Gene: chi-1
C/Keywords: glycosidase; hydrolase

ALIGNMENTS

Query Match		32.5%;	Score 1008.5;	DB 2;	Length 525;
Best Local Similarity		38.4%;	Pred. No. 2.2e-55;		
Matches 211;		Conservative 93;	Mismatches 187;	Indels 59;	Gaps 13;
QY	8	LSIMACIGLMNASIKRD-HNDYSKNPMRIVCVGTWSVYHKVD-PYTIEDIDPFKCTHLM	65		
DB	5	VGVLVLVAFAAAFAEHPKAAASGKKVYCVGTWAVYPCNGRYDIEHIDPSLCTHLM	64		
QY	66	YGFPAIDYKTYIQVDPYQDDNHNHWEKRGYERFNNLRKKNPELTWISLGGWYEGSEK	125		
DB	65	YGFPGINE-DATVRIIDPYLDLEEN-WGRGHIKRFVGLKNVGPGLKTLAAIGMWEGSRK	122		
QY	126	YSDMAANPTYRQQTQSVDLQEQYKFDGLDLDWEYVPGSLGNPKDKNYLALVRELKD	185		
DB	123	FSAAMASGELRRKFISDCVAFQCRHGFQIDLDWYPAQRDGNPLIDNHAQLVEEMRE	182		
QY	186	AFEPHGYLLTAASVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYGWENFYGHNAFLYKR	245		
DB	183	EDDHVGLLLTAASVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYGWENFYGHNAFLYKR	242		
QY	246	PDETDELHYFNVTMYLNGATRKLVGVFPFYGRAMSIDRSKLGKDPAGKMSF	305		
DB	243	SADTTDRLQINNVNASIHFWLAQGGCTGRKVLGIPLYGRNFTLAGAANTQIGAPTGGGT	302		
QY	306	PGFISGEQVLSYIELCQLFQKEEWHIQYDEYNNAPYGVNDKIWYGYDDLASISKLAPL	365		
DB	303	VORYTREPQWNGYNEFCEKLAATEAWDLRWSEQQPYAVRNQWVGYYDLRSVQLKVKYL	362		
QY	366	KELGVGVVWVWLENDDFKHC-GPKNPLNKNVNMINGDEKNSFECILGRTTPTTPTT	424		
DB	363	LQOGLGAVWVWLENDDFKHC-GPKNPLNKNVNMINGDEKNSFECILGRTTPTTPTT	413		
QY	425	TPTT	484		

Db 414 APTT-----STVAGCTTTTTPGANPGTTQPPT--SDAPNHTTTTTEGNGFTTRPPSG 466
QY 485 TTTEHTSETPKYTTTVDGHLKCY--KEGDIPHPTNIHKYLV-----EFVNGGWVH 535
Db 467 -----DG-----PCAGGRYGFVPHPTNCARYICTADTYVEFT----- 500
QY 536 IMPCPPPGTIW 545
Db 501 ---CPFGILF 507
RESULT 2
T14075
chitinase (EC 3.2.1.14) - yellow fever mosquito
C:Species: Aedes aegypti (yellow fever mosquito)
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: T14075
R:de la Vega, H.; Specht, C.A.; Liu, Y.; Robbins, P.W.
Insect Mol. Biol. 7, 233-239, 1997
A:Title: Chitinases are a multi-gene family in Aedes, Anopheles, and Drosophila.
A:Reference number: Z17872
A:Accession: T14075
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1635
A:Cross-references: EMBL:AF026492; NID:G2564720; PID:G2564721; PIDN:AAB81850.1
C:Genetics:
A:Gene: CHT2
A:Introns: 462/3; 524/3; 618/1; 951/3; 1151/2
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
Query Match 28.0%; Score 869; DB 2; Length 1635;
Best Local Similarity 34.3%; Pred. No. 4.8e-46;
Matches 196; Conservative 95; Mismatches 196; Indels 84; Gaps 18;
QY 21 IKRDNDYKSNM-----RIVCYGTVSVTHKVD-PYTIEDIPFKCTHLMYFPAKIDE 73
Db 650 INKETSNDENAIESDVDYKVCYFTNMAWYRQNGKYLDPEDIDADLCTHIVYGFVAVL 709
QY 74 YKTYIQVDPYQDDNHSN---EKGYERFNNLRKNPELMTWLSLGGWYEGS-EKYSDM 129
Db 710 DLVVK-----PHDSNADIDNRFYRVEYKCKKKKVT--VAIGWNDSAGKYSRL 759
QY 130 AANPTYROOFIQSVLDFQYKFDGLDLDWEYVPSRLGNPK-----IDKONYLALVRELKD 185
Db 760 VPSAARQKFIADVAFTKYGFDGLDLDWEYVPCVQVDCCKGFSDEKEGASLVVELSQ 819
QY 186 AFEPHYLLTAAVSPGKKIDRAYDIKELNKFDMWVNTYDYGWENFYGHNAPLYKR 245
Db 820 AFKPKGLLSAVSPSKVVDGYDVTLSDYMDWIAVWADYHGWQDKTGHVAPMVEH 879
QY 246 PDETDELHTYFNNTMYLLNGATRDKLUNGVPFYGRAMSIEDRSKLKLDPAKGMSP 305
Db 880 PDDFKT-----FNAFTIHYWIEKGDPRKLVGMGPMYQGSFSLADNKEHGLNAKTYGGGE 936
QY 306 PGFISGEEGVLSIELCQLFQKEEWHIQVEYNN-APYGYNDKIWGVDDLASISCKLAF 364
Db 937 AGESTRARGLSYEELCANIRKMTVARDRKRGMPYAKGDQVQDQWIMRHKEEY 996
QY 365 LKELGVGVMWVSLNDDPKHGCG-PKPNLLNKNVNMINGDEKNSFECIL--GPSSTTPTT 421
Db 997 VKAMGLGGANIALDLDLDFRNLCDCEYELLATINRVLNYPGPRCVLEKEPQREPER 1056
QY 422 PTTTPT 481
Db 1057 PTPRPT 1104
QY 482 PPTTTEHTSETPKY-----TTVDGHLKCYKEGDIHPPTNIHKYLVCFVNGW 532
Db 1105 PTVTTT---NVPSYQEIANEVDEPTCTDGLF-----VPHPTDCNKYICQYK--- 1150
QY 533 WWHIMPCPPGTIW-----CQEKLT 551

Db 1151 -----LCPGGLYWSVDHCDWPQSTNCRNKQT 1176
RESULT 3
A56596
chitinase (EC 3.2.1.14) - tobacco hornworm
C:Species: Manduca sexta (tobacco hornworm)
C>Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 29-Jan-1999
C:Accession: A56596
R:Kramer, K.J.; Corpuz, L.; Choi, H.K.; Muthukrishnan, S.
Insect Biochem. Mol. Biol. 23, 691-701, 1993
A:Title: Sequence of a cDNA and expression of the gene encoding epidermal and gut chitina
A:Reference number: A56596; MUID:93357793; PMID:8353325
A:Accession: A56596
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-554 <KRA>
A:Cross-references: GB:U02270; GB:S64757; NID:G406048; PID:G406049
A:Experimental source: larvae
A:Note: sequence extracted from NCBI backbone (NCBI:136417, NCBI:136418)
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
Query Match 27.0%; Score 838.5; DB 2; Length 554;
Best Local Similarity 35.4%; Pred. No. 9.2e-45;
Matches 208; Conservative 79; Mismatches 210; Indels 91; Gaps 20;
QY 6 AILSIMACIGLMNASIKRDNDYKSNMRYICVYGVTSVYHK-VDPYTIEDIDPFKCTHL 64
Db 3 ATLATLAVLATAV-----QSDSRARIVCVFSNVAVPCVGRYGIEDIPVEKCTHI 55
QY 65 MYGFAKIDYKTYIQVDFPYQDDNHSNWKRGYERNNLRKNPELMTWISLGGWYEGS 124
Db 56 IYFVIGVTEGNSVLLIDPELD-----VDKNGFRNFTSLRSSHPSVKFVWVGWMAEGSS 110
QY 125 KYSDMAANPYROOFIQSVLDFQYKFDGLDLDWEYVPSRLGNPKIDKONYLALVREL 183
Db 111 KYSHWVAQKSTRMSFRSVVSVFLKDYDFDGLDLDWEYVPSRLGNPKIDKONYLALVREL 170
QY 184 KDAF--EPHYLLTAAVSPGKKIDRAYDIKELNKFDMWVNTYDYGWENFYGHNA 241
Db 171 RRAFIRVGKWEITAAVPLANFELMEGYHVPCLQELDAIHVMSYDLRGNWAGFADVHSP 230
QY 242 LYRPPDETDELHTYFNNTMYLLNGATRDKLUNGVPFYGRAMSIED----- 290
Db 231 LYRPHD-QWAVEKLVNDGLHLWEKGCPSNKLUVGIFPYGRSFTLSAGNNYGLGTFI 289
QY 291 RSKLKLGDPAKGMSPPGFISGEEGVLSIELCQLFQKEE--WHIQVEYNNAPYGYNDKI 348
Db 290 NKEAGGDDPAPYTNATGF-----WAYEICTEVDKDDSGMTKQWDEQKCFYAYKGTQ 342
QY 349 WVGVDLASISCKLAFKELGVSGVMVWSLENDDFKHCPCPKNPLNKNVNMINGDEKNS 408
Db 343 WVGVEOPRSVEIKONWIKQKYLGAWTWALDMDDFQGLCGEKPLIKILHKMS----- 396
QY 409 FECILGPSSTTPTPTPTPTPTPTPT-----TTPTPS-----PTTPTTPTPTPTPTT 456
Db 397 -----SYTVPPPHENTTPTPEWARPSTPSDPSGDPITPTTTAKASITKTIVKIT 449
QY 457 TPTTPTPTPTPT-----PTP-TPTPTAPTPTPTPTTTEHTSETPKYTYVDGHLI 505
Db 450 TTTTAKPPQVIDBENDINVRPEPKPEPEPEVEVP-PTENE-----VDGSEI 497
QY 506 KCYKEGD-IPHTNINIKYLVCFVNGWVWHIMPCPPGIWCOEKLTC 552
Db 498 -CNSDQYIIPDKKCHKYWRG--VNGE--AMQFSQHGTVFVNVELNVC 540
RESULT 4
A53918
chitinase (EC 3.2.1.14) precursor - braconid wasp (Chelonus sp.)
C:Species: Chelonus sp.
C>Date: 28-Jul-1995 #sequence_revision 28-Jul-1995 #text_change 21-Jul-2000

[illegible]

Qy	188	EPHG-----YLLTAAVSPGKKIDRAYDIKELNKLFDWMVNTYDYHGGWENFYGHNA	240
Db	165	KNEAQUTMRPRLLLSAAVSGDPHVQVQKAEARLLGRLLDFISVLSDYHGSWEKVTGHS	224
Qy	241	PLYKRPDEIDELHTYFNVNTYMHYYLNNGATDKLVMGVVPFYGRAWSIEDRSKIKLGDP	300
Db	225	PLFSLPGDPK-----SSAYAMVYWRQLGVPEKLLAGLPTYGRTHLLKASQNELRAQ	278
Qy	301	KGMSPPGFTSGEGVLSYIELCOLPQKEWHIQVDEYYNAPYGYNDKIWVGYDDLASIS	360
Db	279	VGPASPGYTKQAGFLAYVEICCFVRRAKKEWINDQY--VPYAFKGKEWGYDDAISFGY	336
Qy	361	KLAFLKELGVSGMVWSLENDPFKH-CGP-KNPLLANKVHNMINGDEKSFECILGPSTT	418
Db	337	KAFPIIKREHFGGAMVWTLDDDFRGYFCGTGPFPLVHTLANNLLVNDFFSS-----	386
Qy	419	TTPT-----TTTPTPTPTPTPTPTPTPTPTPTPT-----TTTPSTTTPTPTPTPT	466
Db	387	TPSPKWFSTAVNSSRIQPEMTMTREDLTTGLGILPGGEAVATEHRSKETWTITPKGE	446
Qy	467	TPPT-TP-----TPAPTSTPSP-----TTTHTSETP	494
Db	447	IATPTPLSFRGHTAAPEKTESPGKPLTIVGHLAVSP	486
RESULT 7			
I46470			
estrogen dependent oviduct protein precursor - sheep			
C/Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)			
C/Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 05-Nov-1999			
C/Accession: I46470			
R/DeSouza, M.M.; Murray, M.K.			
Endocrinology 136, 2485-2496, 1995			
A/Title: An estrogen-dependent secretory protein, which shares identity with oviduct and embryo development			
A/Reference number: I46470; MUID:95269691; PMID:7750470			
A/Accession: I46470			
A/Status: preliminary; translated from GB/EMBL/DBJ			
A/Molecule type: mRNA			
A/Residues: 1-539 <DES>			
A/Cross-references: EMBL:U16719; NID:g885600; PIDN:AAC48471.1; PID:g885601			
Query Match 22.0%; Score 685; DB 2; Length 539;			
Best Local Similarity 33.8%; Pred. No. 3.2e-35;			
Matches 173; Conservative 90; Mismatches 185; Indels 64; Gaps 17			
Qy	10	IMACIGLWASIKRDHNDYKSNPMELVCYGVGTWSYVHKVDPTYI--EDIDPFKCTHLMYG	67
Db	4	LLUWVLG---LMLKHDGAH--KLVCYFTNWA-FSRPGSASTLPRLDLPFLCTHLVFA	57
Qy	68	FAKIDBYKTYIQVDFPYQDDNHSWEKRGYRFNNLRKPNELTMTISLGGWEGSEKYS	127
Db	58	FASWNNQ--IVPKDPLD-----EKILYEFENKLEKRNRLGLTLLSVGWNFGTSRT	108
Qy	128	DMAANTFYQQFTQSVLDFQBYKFDGLDWEYVPGSELGNPKTDKQNYALVRELKDAP	187
Db	109	KMLSTFSNRRFVKSVIALLRTHGPDGLDPLFLYPGLR-GSPARDRWTFVFLLEELQAF	167
Qy	188	EPHG-----YLLTAAVSPGKKIDRAYDIKELNKLFDWMVNTYDYHGGWENFYGHNA	240
Db	168	KNEAQUTMRPRLLLSAAVSGDPHVQVQKAEARLLGRLLDFISVLSDYHGSWEKVTGHS	227
Qy	241	PLYKRPDEIDELHTYFNVNTYMHYYLNNGATDKLVMGVVPFYGRAWSIEDRSKIKLGDP	300
Db	228	PLFSLPGDPK-----SSAYAMVYWRQLGVPEKLLAGLPTYGRTHLLKASQNELRAQ	281
Qy	301	KGMSPPGFTSGEGVLSYIELCOLPQKEWHIQVDEYYNAPYGYNDKIWVGYDDLASIS	360
Db	282	AGPASPGYTKQAGFLAYVEVCSFVQRAKRWINDQY--VPYAFKGKEWGYDDAISFGY	339
Qy	361	KLAFLKELGVSGMVWSLENDPFKH-CGP-KNPLLANKVHNMINGDEKSFECILGPSTT	418
Db	340	KAFPIIKREHFGGAMVWTLDDDFRGNGFCGTGPFPLAHTLNNLLVNDFFSS-----	389

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Qy 419 TPTP-----TTTTTTTPTTTPSPPTTPSPPTP-----TTTTPTTPTTTPSPT 466
Db 390 TSPSKFWFTAVNSSRRIGPEMTMDRLTGILGLGGEAVATETHRKSATMTTTPRGE 449
Qy 467 TPTPT-TP-----TPAPTSTPSPTTEHTS 491
Db 450 TATPTTTLSSGRRTAAPGKTESPGKPLTS 481

RESULT 8
I38605
Oviductal glycoprotein - human
C:Species: Homo sapiens (man)
C>Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 29-May-1998
C:Accession: I38605
R:Arias, E.B.; Verhage, H.G.; Jaffe, R.C.
Biol. Reprod. 51, 685-694, 1994
A:title: Complementary deoxyribonucleic acid cloning and molecular characterization
A:Reference number: I38605; MUID:95119256; PMID:7819450
A:Accession: I38605
A>Status: preliminary; translated from GB/EMBL/DDDBJ
A:Molecule type: mRNA
A:Residues: 1-654 <RES>
A:Cross-references: EMBL:U09550; NID:g529147; PID:g529148

Query Match      21.5%; Score 668; DB 2; Length 654;
Best Local Similarity 33.1%; Pred. No. 4.7e-34;
Matches 176; Conservative 91; Mismatches 192; Indels 72; Gaps 19;

Qy 10 IMACIGLMNASIKRDNDXSKNPMRVYCVGTWSVHKVDPYTI--EDIPFKOTHLMYG 67
Db 4 LLWLWGLV--LVLKHDGAH--KLVCYTNA-HSRPGASILPHDLDPFLCTHLIFA 57
Qy 68 FAKIDEKYTYIQVDFPYQDDNHSWEKRGVERNNLRNLKNEPLTTMISLGWVEGSEKYS 127
Db 58 FAGMNNOI---VAKDLQD-----EKILYPEFNKLERNELKTLISIGWNFGTSRFT 108
Qy 128 DMAANTYRQQFQSVLDLFLOEYKFQGLDLDWEYPGSRIGNPKIDKQYLALVRELKDAF 187
Db 109 TMLSTPANREKKFIASVISLARTDFGLDLFFLYPGLR-GSPMHDRWTFLFLIELLFAF 167
Qy 188 EPHG-----YLLTAASPGDKIDRAYDINKELNKLFDMMVMVTYDHGGWENFYGHNA 240
Db 168 RKBALTMRPRLLSRAVSVPHVQTSYDVRFGLRLDFINVLSYDLHGSWERTGNS 227
Qy 241 PLYKRDETDDELHYTFNVNTMYHYLNNGATRKLVMGVFPFYGSRAWIEDRSKLKLGDP 300
Db 228 PLFSLPEDPK-----SSAYAMNYWRKLGAPSEKLIINGIPTYGRTPELLKASKNQLQARA 281
Qy 301 KMSPPGFTSGEGVLSYIELCOLF--QKEWHIQDYDEYNAPGYNDKIWVGYYDDLASI 358
Db 282 IGPASPGKYTKQEGFLAYFEICFSVMGAKKHV----IDYQVVPYANKGKWGVYDNATSF 337
Qy 359 SKCLAFELKELGVGMVWSLENDDFKG-HCGP-KNPILLKVHNMINDEXNSFCILGPS 416
Db 338 SYKAWPTRRHFGAGMWYTLDMDDVRGTCGTGFPLVYLINDLIVRAEPS-----S 389
Qy 417 TTTPT-PTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPT 466
Db 390 TSIPQFWSAVNSSTDPERLATVTTAWTTDSKILPPCGAGVTEIHGKCENWITTRGTT 449
Qy 467 TPTPTTPT-----PAPTTSTPSTTTTHTSETP--KYTTTVVDGH 503
Db 450 TVPTKETVSLGKHVALGKETITGAMTWTSVGHQSMTPEGKALTPTV-GH 499

RESULT 9
A49562
cartilage glycoprotein gp39 precursor - human
N:Alternate names: 39K synovial protein
C:Species: Homo sapiens (man)
C>Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 22-Jun-1999

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C;Accession: A49562; S10677; A33162
R;Hakala, B.E.; White, C.; Recklies, A.D.
J. Biol. Chem. 268, 25803-25810, 1993
A;Title: Human cartilage gp-39, a major secretory product of articular chondrocytes and
A;Reference number: A49562; MUID:94064658; PMID:8245017
A;Accession: A49562
A;Status: preliminary
A:Molecule type: mRNA
A;Residues: 1-383 <HAK>
A;Cross-references: GB:M80927; NID:g348911; PIDN:AAA16074.1; PID:g348912
Biochem. J. 269, 265-268, 1990
A;Title: Human synovial cells secrete a 39 kDa protein similar to a bovine mammary proteo
A;Reference number: S10677; MUID:90328983; PMID:2375755
A;Accession: S10677
A:Molecule type: protein
A;Residues: 22-40,'X',42-45 <NY2>
C;Superfamily: Streptomyces chitinase chi40
C;Keywords: cartilage; extracellular protein; glycoprotein
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-383/Product: cartilage glycoprotein gp39 #status predicted <MAT>

Query Match 21.3%; Score 662; DB 2; Length 383;
Best Local Similarity 34.9%; Pred. No. 5.5e-34;
Matches 144; Conservative 81; Mismatches 136; Indels 52; Gaps 12;

Qy 2 KTIYAILSIMACIGLMMNASIKRDNDYSKNPMRIVCYGVTSVYHKVDPTYIED-IDPFK 60
:
Db 7 QTGEWLVLLQQ-----SAYKLVCYTWSQYREGDSCFPDALDRFL 50

Qy 61 CTHLMYGFAKIDEKYITQIVDPYODDNHSWEKRG---YERFNLRKLNPELTMTMISLG 117
:
Db 51 CTHIIVSFANI-----SNHDITWENDVTLYGMLNTLKRNPNLKTLLSVG 97

Qy 118 GWTEGSEKYSDMAANPTROOFTQSVLDFLOEYKFQGLDLWDYPSRLGNPKDKONYL 177
:
Db 98 GWNGFSQRFKIASNTOSRETFIKSVPPFTRTGHFGDLAWLPYGR-----DKQHFT 151

Qy 178 ALVRELKDAF-----EP--HGVLITAAVSCKDIKDRAVDKEINKLFDMWNVTYDHVG 231
:
Db 152 TLTKMKAEFIKENAQKKQLLSAUSAGKVTDSSDYAKISQHLDFISIMTYDFHGA 211

Qy 232 WENFYGHNAPLYKRDETDLHYFNVNMYHYLNNGATRDCLVMGVPPFYGRAWSIEDR 291
:
Db 212 WRGTGGHSLP-F-RGQEDASPDSPSTNDYAVGYMLALGAPASKLVMGIPPTFGSGFTLAS- 269

Qy 292 SKULGDPAKMSPPGISBEGVLSYIEICQLFQKEWHIQYDEVYNAPYGVNDKIWVG 351
:
Db 270 SETCVGAPISGPGIPGRFTKEAGTLAYEICDFELRGATVHRTLEG--QVPYATKGQWVG 327

Qy 352 YDDLASTISKLAFLKELGVSGWMVSWLENDDFKG-HCGP--KNPLLNKHVNMI 401
:
Db 328 YDDQESYKSVQYLKDRQLAGAMVVALDLLDFQGSFCGQDLRFPLTNKDAL 380

RESULT 10
S51327
heparin-binding glycoprotein 38k - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 22-Jun-1999
C;Accession: S51327
R;Shackelton, L.M.; Mann, D.M.; Millis, A.J.T.
submitted to the EMBL Data Library, January 1995
A;Description: Identification of a 38kDa heparin-binding glycoprotein (gp38k) in differ
A;Reference number: S51327
A;Accession: S51327
A;Status: preliminary
A:Molecule type: mRNA
A;Residues: 1-383 <SHA>
A;Cross-references: EMBL:D47803; NID:g634097; PIDN:CAB87764.1; PID:g634098
C;Superfamily: Streptomyces chitinase chi40

Query Match 20.9%; Score 650; DB 2; Length 383;

```

Qy 150 YKFDGLDLDWEYFGSRLGNPKIKQNYALVRELKDAF-----BP--HGVLTTAAVSPGKD 203
Db 131 YQFDGLDLAWLPRLR-----DKQYFSTLTKELNAEFTKEVQFGREKLLLSAALSAGKV 184
Qy 204 KLDRAVDIKELNKLDFMNMVMTYDVHGWNFYGHNAPLYKRPDETDLHLYFNVNYTMH 263
Db 185 AIDTGYDTAQIAQHLDFFINLMTYDFHGWRRQITGHSPLFQGGKOT-RRFRYSNNYAVQ 243
Qy 264 YYLNNAGATRDKLVMGVPPFYGRAWSIEDRSKLGDPAKGMSPGPFISGEGVLSYIELCQ 323
Db 244 YNTRLCAQAQSKLLMGIPITFGKSFTLAS--SENQLGAPISGEGLPGRFTKEAGTLAAVEICD 302
Qy 324 LQKQEEWHIQDEYNNAPYGVNDKIWGVYDDLASISCKLAFLIKELGVSGV----WVWSLE 379
Db 303 FLKGAEVVHRLSNE--KVPFATKGNQWVYGEDKESVKNKGVGLKEKCLAGAGCHWIMWI- 359
Qy 380 NDDPKFHGCGPKNPLLNKVHNNINGDEKNSPECILGPSTTTPTPTTTP 426
Db 360 ----SGHCOPKN-----SSRSFTFSRMP 378

RESULT 12
S27879
C:Species: Mus musculus (house mouse)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 22-Jun-1999
C:Accession: S27879
R:Chang, N.C.A.; Liu, C.H.; Chang, A.C.
submitted to the EMBL Data Library, June 1992
A:Description: Molecular characterization of a secretory protein (YM-1) trans-
A:Reference number: S27879
A:Accession: S27879
A:Molecule type: mRNA
A:Residues: 1-399 <CHA>
A:Cross-references: EMBL:M94584; NID:g202441; PIDN:AA562394.1; PID:g202442
C:Superfamily: Streptomyces chitinase ch40
F:1-21/Domain: signal sequence status predicted <SIG>
P:22-399/Product: secretory protein YM-1 #status predicted <MAT>

Query Match 19.6%; Score 608; DB 2; Length 399;
Best Local Similarity 36.3%; Pred. No. 1.3e-30;
Matches 141; Conservative 67; Mismatches 140; Indels 40; Gaps 14

Qy 34 RIVCYVGTWSVTHKVD-PYTTIEDIPFKCTHLMTGPAKI--DEYKTIQVDFPYQDDNNH 90
Db 23 QLMCYVTSWAKDRPIEGSFKGNIDPCLTCTLLIYAFAGMQNNIEITYT-----H 70
Qy 91 SLMKCYVERFNNLR-LKNPELTTMISLGGWYEGSEKYSDMAANTYRQOFIOSVILDFLOE 149
Db 71 EQDLRDYEALNGDKOKKTEKLLIAIGWFGGAPFSAMVSTPQNRQIFQSVIRFLRQ 130
Qy 150 YKFDGLDLDWEYFGSRLGNPKIKQNYALVRELKDAFEPHG-----YLLTAAVSPGK 202
Db 131 YNFDGLNLQWYQGSNR-GSPKDKHLFSLVKEMKFAFEESVEKDIPLLIT---STGA 186
Qy 203 DKIDRAYD-IKELN--KLFDMNMVMTYDVHGWNFYGHNAPLYKRPDETDLHLYFNVN 259
Db 187 GIIDVTKSRTSLNCLSLDDYIQNVYDLDHPDKDGYTGENSEPLKSPYDIGK-SADLAVD 245
Qy 260 YTHHYLLNNGATRDKLVMGVPPFYGRAWSIEDRSKLGDPAKGMSPGPFISGEGVLSYI 319
Db 246 SIISYWKDHGAASEKLITVGPAYHTFTLSDPSKTGTGAPITSTGPPGKYTDSGLUATY 305
Qy 320 ELCOLFPQK---BEWHIQDEYNNAPYGVNDKIWGVYDDLASISCKLAFLIKELGVSGWVW 376
Db 306 EVCTFLNEGATEW---DAQEVFYAQGNWGYNDVRFSKLKAQWLKNNLGGAVVW 361
Qy 377 SLENDPFKG-HCGPKN-PLNLKVHNNIN 402
Db 362 PLMDDDFSGSFCHQRHFFPLTJTKGDLN 389

```

A38221
chitinase (EC 3.2.1.14) MF1 - nematode (Brugia malayi)
C:Species: Brugia malayi
C:Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
C:Accession: A38221
R:Fuhrman, J.A.; Lane, W.S.; Smith, R.P.; Piessens, W.F.; Perlier, F.B.
Proc. Natl. Acad. Sci. U.S.A. 89, 1548-1552, 1992
A:Title: Transmission-blocking antibodies recognize microfilarial chitinase in brugian l
A:Reference number: A38221; MUID:92179220; PMID:1542646
A:Accession: A38221
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid; protein
A:Residues: 1-504 <FTH>
A:Cross-references: GB:W73689; NID:g156063; PID:AAA27854.1; PID:g156064
A:Note: sequence extracted from NCBI backbone (NCBIP:85345)
C:Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 19 54; Score 604.5; DB 2; Length 504;
Best Local Similarity 30.14; Pred. No. 36-30; Indels 69; Gaps 17;
Matches 156; Conservative 86; Mismatches 208;

Qy 37 CYVGTWVTHKVD--PYTIEDIDPKCTHLMYGFKAKIDYKTYIQVDFPYQ--DDNHNSWEK 94
Db 27 CYITNMQAYRDEGEKFLPGNIPNGLICHTILYAFKVD---LGDSKPFWNDEDETSWK 82
Qy 95 RGVRFNNLRUKNELTMTISLGMWEGSEKYSKDVAAAPTQYQQIQSVLDFLQYKFDG 154
Db 83 GMSAVTKLRETNPLKVLISYGVGVNFGSAIFTGTIAKSAKTERPIKGAIAFLRNKDFG 142
Qy 155 LLDLWEYP--GSLGNPKIDKQNYLAVRELDAEPHYGLLTAAVSPGKDKIDRAVDIKE 213
Db 143 FDLDEYFVPGVAESHAKLVEAMKTAFAEEAKTSGKQR--LLLTAAVSAAGKTIIDGSYNVES 201
Qy 214 LNKLFDMVNAVMTYDHGWNPFYGHNAFLYKRPDTEBLHTYFNVNMYTHYLNNGATRD 273
Db 202 LGKNFDLLFLMSYDLHGSWEKNVDLHGKLTKEVSGI--GIENTEFAADYWASKMPKE 260
Qy 274 KLVNGVPFYGRAWSIEDRSKLKLDGPAKGMPPGPFISSEGVLSYIELCOLFQKEWHIQ 333
Db 261 KIITGIPMQAGWTLDPNSETAIGAAASRPSSAKTNPAGGTASYWEICKYLKEGGKETV 320
Qy 334 YDEYNAPYGVNDKIWGVYDDLASISCKLAFLKELGVSGVMVWSLENDFKG--HCGP--KN 391
Db 321 HOEGVGA--YMWGDCWYGVNEETIRIKMKLKEKGYGGAFIWALEDFFDTGKSCGKGPY 379
Qy 392 PLLKVNMMINGDEKNSPECILGSPSTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPT 451
Db 380 PLINAISSLEGESEN-----PEITTEESITETAYETDETEE----- 418
Qy 452 TTPSPT 507
Db 419 -----TSETAYDTD-----ETSETSET--EATTYTDTDETEG--EC 451
Qy 508 -YKEGDIPHNTNIHKYLVCFVNGVGGWVHIMPCPGTIW 545
Db 452 PERDGLFPHTDCHLFIQC-----ANNIAYVMOCPATTF 486

RESULT 14
D83764
chitinase B90916 [imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C:Accession: D83764
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hirano
Nucleic Acids Res. 28, 4317-4333, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: A83650; MUID:20512582; PMID:11058132

RESULT 14

D83764
 Chitinase BH0916 [imported] - Bacillus halodurans (strain C-125)
 C:Species: Bacillus halodurans
 C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
 C:Accession: D83764
 R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hirano, S.
 Nucleic Acids Res. 28, 4317-4331, 2000
 A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
 A:Reference number: AB3650; MUID:20512582; PMID:11058132
 A:Accession: D83764
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-599 <STO>
 A:Cross-references: GB:AP001510; GB:BA000004; NID:gi10173440; PIDN:BA004635.1; GSPDB:GN001

RESULT 13

A: Experimental source: strain C-125

C: Genetics:

A: Gene: BH0916

Query Match 19.1%; Score 592; DB 2; Length 599;
Best Local Similarity 29.0%; Pred. No. 2.3e-29;
Matches 183; Conservative 98; Mismatches 216; Indels 134; Gaps 29;

```
QY 2 KTIYAILSIMACIGLMNASIKRHNHNSKPNRIVCVGTWVSYYHKVDYTTIEDIDPFKC 61
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 9 KLLIWIWTVLLVWTPADQVGAETSDDQYKIVAYPSWAGYGR--DYQVMDIDASKI 66
QY 62 THLMYGFAG-----IDYKVTIQVDFPYQD-----DNH 89
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 67 SHNYAFANICWGRHGNPDAGNPQTWSCODENGIVDPNGSIVMGDFWIDAQKSNFG 126
QY 90 NSWEK--RG-YERFNNLRKLNKPNLTWISLGGHYEGSEKYSDMAANPTVRQFIOQLVDF 146
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 127 DTWDEPLRGNFQKQINKKEHPHLKLLISVGGH-TWSNRFSDMAATKETRENFANSAPF 185
QY 147 LOBYKFDGLDWEYP--GSRIGNPK--IDQNYLALVRELKDAPEPHG-----YLLTPA 196
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 186 IRKYGFQVDVDWEYFVSGGLPGNSRRPDKENHVLLOEVRDKLDEAGQEDGKYLLTI 245
QY 197 A--VSPGKOKIDRAYDIKELNKLFDWNNVTYDHGWNENFYGHNAPLYKRPDETD-ELH 253
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 246 ASGASPGYVENNK---LNEIAETVDNINIMTYDFNGWQWISGHNAPLYDPATANTELP 302
QY 254 T--YFNNVTMYYLNNGATRDKLVMGVPEYGRAMSTEDRSKLGDPKAGMSPPGFISG 311
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 303 TPSEHFNVESAVEGHLQAGVFEHLVLGMPPYGRGWSNCDGA--NQGEYQR-CAPPREGTW 359
QY 312 EBGVLSVIELCOLFQKEWHIQ--YDEYN---APYGN--DKIWWGVDDILASISCKL 362
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 360 ENGUFFESDL-----EDHVNKNGQRYNDVAKVPLNATNGNFIYDDSESPRYKT 413
QY 363 AFLKELGVSGVMVMSLENDDFKHCGRKPNLLKNVNMINGDEKNSFECILGSPSTTPTP 422
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 414 DFIKSNLAGSMFWDVSGDR-----NGTLTALADQLG---FTPHE 451
QY 423 TTTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPT 476
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 452 GQPEEPSAPTNIQATEVSTVTLTWQAPTBEPTQSVAYDSKEKTTHTTTITIEDLQ 511
QY 477 PTTSTPSPTTTEH-----TSETPKVTYVDG-----HLIKCYKEGD-IPHTNI 519
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 512 PETTYTFVSAEHKQGRHAGALQVTTKSETGGDGTAPTWOANNVYTGDDQVQHGKGL 571
QY 520 HKYLVCBFVNGWVWVHMPCPGT-----IW 545
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 572 YE-----AKWWT--TGEPGTGEGWVW 592
```

RESULT 15

A38368

Chitinase (EC 3.2.1.14) precursor - Bacillus circulans

C: Species: Bacillus circulans

C: Date: 28-Jun-1991 #sequence_revision 28-Jun-1991 #text_change 15-Oct-1999

C: Accession: A38368

R: Watanabe, T.; Suzuki, K.; Oyanagi, W.; Ohnishi, K.; Tanaka, H.

J. Biol. Chem. 265, 15659-15665, 1990

A: Title: Gene cloning of chitinase A1 from Bacillus circulans WL-12 revealed its evolution

A: Reference number: A38368; MUID: 90368776; PMID: 2203782

A: Accession: A38368

A: Status: preliminary

A: Molecule type: DNA

A: Residues: 1-699 <WAT>

A: Cross-references: GB:M57601; GB:J05599; NID:gl066341; PIDN:AAA81528.1; PID:gl42688

C: Superfamily: fibronectin type III repeat homology

C: Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match

Best Local Similarity 18.1%; Score 561; DB 2; Length 699;

29.4%; Pred. No. 2.3e-27;

```
Matches 170; Conservative 67; Mismatches 185; Indels 156; Gaps 23;
QY 34 RIVCVGTWVSYYHKVDYTTIEDIDPFKC THLMYGFAG----- 71
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 45 KIVGYFPSWAGYGR--NYNVAIDPTTKVTHINYAFADICWNGIHGNDPSPGNPVTWTCQ 102
QY 72 DEYKVTIQV-----DDPYQDDNH---NSWEK--RGYERFNNLRKLNKPNLTWISL 117
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 103 NEKQTTINPVTIVLGDWIDTGTGTAGTWDQDIAGNINQLNKLKQTNLNLTIISVG 162
QY 118 GWYEGSEKYSDMAANPTVRQFIOQLVDFLOEYKFDGLDWEYF--GSRIGNPK--IDK 173
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 163 GW-TWSNRFSDVAATAATREVFANSADVFLRKYNFDGVLDWVEYFVSGGLDGNKSRPEDK 221
QY 174 QNYLALVRELKDAPEPHG-----YLLTAAPVSPGKOKIDRAYDIKELNKLFDWNNVTYD 227
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 222 QNYTILLSKIREKLDAAGAVDGKYYLLTIA--SGASATVAAANTELAATAAIVDWINIMTYD 280
QY 228 YHGWNENFYGHNAPLYKRPDET---DELHTYFNNVTMYYLNNGATRDKLVMGVPEY 283
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 281 FNGAWQKISAHNAPLNVDPAASAAGVDPDANT--FNVAAGAQQHLDAGVPAAKLVLGVPFY 339
QY 284 RAWSTEDRSKLGDPKAGMSPPGFISGEGLSVIELCOLFQKEWHIQ---YDEYN- 339
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 340 RWDGCAQAGNGQYQTCGGSSVG--TWEAGSFDFYDL-----EANYINKNGYTRYWND 391
QY 340 ---APYGN--DKIWWGVDDILASISCKLAFELKELGVSGVMVMSLENDDFKHCGRKPNLL 394
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 392 TAKVPEYLYNASNKRPFISYDDAESVGKYTAYIKSKGLGAMFWELSGDRNK----- 441
QY 395 NKVNMINGDEKNSFECILGSPSTTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPT 436
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 442 -TLQNKLKAD-----LPTGGTVPVDDTTAPSVPGNARSTGVTANSVTLAWN 486
QY 437 -----SPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPT 458
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 487 ASTDNVGTGVNVNNGANLATSVTGTTATISGLTAGTSYFTTIKAKDAAGNLSAASNAVT 546
QY 459 PTTTPTSP--TTPTPTPTPTP--APTSTPTPTPTTTEHTSET 493
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 547 VSTTAQPGDQAPTAPTNLASTAQTTSSTITLSWTAST 584
```

Search completed: March 22, 2004, 07:01:28

Job time : 37.0951 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 22, 2004, 06:31:13 ; Search time 21.2868 Seconds
(without alignments)
1357.597 Million cell updates/sec

Title: US-09-662-293-15

Perfect score: 3107

Sequence: 1 MKTIYAILSIMACIGLMNAS.....IMPCPPGTWCQEKLTGICE 555

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	838.5	27.0	554	1	CHIT MANSE
2	738	23.8	465	1	CHT1_HUMAN
3	734.5	23.6	473	1	CHIA_MOUSE
4	723	23.3	508	1	CHIL_DROME
5	708.5	22.8	476	1	CHIA_HUMAN
6	705.5	22.7	617	1	CHIT_CABEL
7	696.5	22.4	527	1	OGP_FIG
8	685.5	22.1	537	1	OGP_BOVIN
9	685	22.0	539	1	OGP_SHEEP
10	680	21.9	381	1	C3L1_MOUSE
11	680	21.9	671	1	OGP_MESAU
12	680	21.9	721	1	OGP_MOUSE
13	668	21.5	678	1	OGP_HUMAN
14	662	21.3	383	1	C3L1_HUMAN
15	654.5	21.1	623	1	OGP_PAPAN
16	630	20.3	390	1	C3L2_HUMAN
17	611.5	19.7	396	1	CHT1_MOUSE
18	604.5	19.5	504	1	CHIT_BRUMA
19	576	18.5	458	1	CH13_DROME
20	561	18.1	699	1	CH11_BACCI
21	411	13.2	423	1	CH14_TRIHA
22	410.5	13.2	423	1	CH11_APHAL
23	407.5	13.1	563	1	CHIA_SERMA
24	384	12.4	820	1	CHIA_ALTSO
25	377.5	12.1	550	1	CH10363_oryzia_pseu
26	360.5	11.6	551	1	CHIT_NPVAC
27	353	11.4	499	1	CHIB_SERMA
28	341	11.0	619	1	CHIT_STRLI
29	339.5	10.9	427	1	CH11_COCPO
30	326	10.5	610	1	CHIT_STRLP
31	280	9.0	1046	1	CH1D_VIBFU
32	266.5	8.6	474	1	VTP3_TTVIV
33	259	8.3	5179	1	MUC2_HUMAN

ALIGNMENTS

RESULT 1

CHIT MANSE

ID CHIT MANSE STANDARD; PRT; 554 AA.
AC P36362;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Endochitinase precursor (EC 3.2.1.14).
OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Sphingioidea;
OC Sphingidae; Sphinginae; Manduca.
OX NCBI_TaxID=7130;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93357793; PubMed=8353525;
RA Kramer K.J., Corpuz L., Choi H.K., Muthukrishnan S.;
RT "Sequence of a cDNA and expression of the gene encoding epidermal and gut chitinases of Manduca sexta.";
RL Insect Biochem. Mol. Biol. 23:691-701(1993).
RN [2]

SEQUENCE FROM N.A.

RP MEDLINE=97215580; PubMed=9061927;
RX Choi H.K., Choi K.H., Kramer K.J., Muthukrishnan S.;
RA "Isolation and characterization of a genomic clone for the gene of an insect molting enzyme, chitinase.";
RL Insect Biochem. Mol. Biol. 27:37-47(1997).
CC -!- FUNCTION: Digest chitin in the exoskeleton during the molting process.
CC -!- CATALYTIC ACTIVITY: Hydrolysis of the 1,4-beta-linkages of N-acetyl-D-glucosamine polymers of chitin.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Epidermis and gut.
CC -!- DEVELOPMENTAL STAGE: High levels seen in the epidermis on day 0, but rapidly disappears and is undetected on days 1-4 of fifth instar. It reappears on day 5 and peaks on day 7 after which a rapid decline is seen. In the gut is detected on day 6 with lower levels seen on days 0, 7 and 8.
CC -!- SIMILARITY: Belongs to chitinase class II (family 18 of glycosyl hydrolases).
CC -!- SIMILARITY: Contains 1 chitin-binding type-2 domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U02270; AAC04924.1; -
CC EMBL: L49234; AAB53952.1; -
CC PIR: A56596; A56596.
CC InterPro: IPR002557; Chitin_bind_Pera.
CC InterPro: IPR001223; Glyco_Hydro_18.
CC InterPro: IPR001579; Glyco_hydro_18AS.
CC -----

34 247 7.9 1513 1 MUC2_RAT
35 244 7.9 662 1 MUC1_XENLA
36 238 7.7 279 1 Y091_NPVOP
37 230 7.4 400 1 MUA1_XENLA
38 227.5 7.3 1331 1 MANB_CALSA
39 221 7.1 267 1 EXTN_MAIZE
40 217.5 7.0 544 1 GP10_DICDI
41 217.5 7.0 1161 1 DANA_YEAST
42 215.5 6.9 705 1 GUN6_DICDI
43 215.5 6.9 1146 1 KTXA_KLULA
44 208.5 6.7 283 1 EXTN_SORBI
45 207 6.7 307 1 SGS3_DROME
Q62635 rattus norv
Q05049 xenopus lae
O10341 oryza pseu
P10667 xenopus lae
P22533 caldocellum
P14918 zea mays m
Q06885 dictyostell
P47179 saccharomyc
P22699 dictyostell
P09805 kluyveromyc
P24152 sorghum bic
P02840 drosophila

```
DR Pfam; PF01607; CBM_14; 1.
DR DR PF00704; Glyco_hydro_18; 1.
DR Predom; P0000471; Glyco_hydro_18; 1.
DR SMART; SM00494; ChitB2; 1.
DR DR SMART; SM00636; Glyco_18; 1.
DR DR PROSITE; PS00940; CHIT BIND II; 1.
DR DR PROSITE; PS01095; CHITINASE 18; 1.
KW Hydrolase; Glycosidase; Chitin degradation; Chitin-binding; Signal;
KW Glycoprotein.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 554 ENDOCHITININASE.
FT DOMAIN 396 453 SER/THR-RICH.
FT DOMAIN 495 553 CHITIN-BINDING TYPE-2.
FT ACT_SITE 146 146 PROTON DONOR (BY SIMILARITY).
FT CARBOHYD 85 85 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 303 303 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 407 407 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 545 545 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 554 AA; 62203 MW; 3989D756C96CD490 CRC64;

Query Match 27.0%; Score 838.5; DB 1; Length 554;
Best Local Similarity 35.4%; Pred. No. 6.3e-39;
Matches 208; Conservative 79; Mismatches 210; Indels 91; Gaps 20;

QY 6 ALLSTIMACIGLWNASIKEDNDYDKNPWRIVCYVGTWVSVYHK-VDPYTIEDIDPFKCTHL 64
DB 3 ATLATLAVLATAV-----QDSRRARIVCYFSNWAIVRPGVGRYGIEDIPVEKCTHI 55
QY 65 MYGFAKIDEXKYTIQVDFPYODDNHNSWEKGYERFNNLRNKLNPETLTMISLGGWYEGSE 124
DB 56 IYSGFVTEGSEVLIIDPELD-----VDKNGFRNFTSLRSHSPVRFWVAVGWAGSS 110
QY 125 KYSDMAANPTVYRQFIQSLVDFLOEYKFDGLDWEYEGSR-LGNPKIDKQNYLALVREL 183
DB 111 KYSHVVAQKSTRMSFIRSVSFLKXYDFDGLDWEYFGAADRGSFSDKDKELYLVQEL 170
QY 184 KDAP--BHGVLITAAVPGKDKIDRAYDIKELKLFDMWVWYDVGHWENFYGNAP 241
DB 171 RRAPIRVGKGWELTAAVPLANFRLMGEGYVPELCOELDAIHVMSYDLRGNWAGFADVHSP 230
QY 242 LYKRPDEIDELHTYFNWVTHVYLNNGATDKLVNMGVPEYGRAWSIED----- 290
DB 231 LYKRPD--QWYKLVNVDLHLWEKGPCKNKLWVGIFGRFTLSAGNNVGLGTFFI 289
QY 291 RSKLGLDPKAGKSPGPGISGEEVLSYELCOLFOKEE--WHQYDYYNAPYGYNDKI 348
DB 290 NKEAGGDPAPYTNATGP-----WAYVEICTEVDKDDSGWKNDQGCPCYAYKGTQ 342
QY 349 WGYDDLASISCKLAFKLKELGVSGVWVWSLENDPFKHCGRPNLLNKNVNMINGDEKNS 408
DB 343 WGYEDPRSVELKNNWIKQKQYLGAMTWAIDMDDFQGLCGEKNPLIKILRHMS----- 396
QY 409 FECILGPSTTTPTPTPTPTPTPT-----TPTTPTS-----PTPTTPTSPSTPTPTTSP 456
DB 397 -----SYTVPPPHPTENTPTPEWARPPSPSPSEGDPIPTTTTAKPASTTKTKTKTT 449
QY 457 TPTPTTPTSPSTT-----PTP--TTPPTPTTPTPTTPTTPTTPTTPTTPTTPTTPTT 505
DB 450 TTTTAKPQSVIENDEINREPEKPEQPEVEVTP-PTNE-----VDGSEI 497
QY 506 KCYKEGD-IPHTNIHKYLVCFVNGVWVWVHMPCPGPTIMQCEKILTC 552
DB 498 -CNSQDYIPDKKHCDKYRC--VNGE--AMQFSQHGTVFVNLNVC 540

RESULT 2
ID CHIT1 HUMAN STANDARD; PRT; 466 AA.
AC Q13231: Q9H3V8;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Chitotriosidase 1 precursor (EC 3.2.1.14) (Chitinase 1).
```

```
GN CHIT1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), FUNCTION, AND SUBCELLULAR
RP LOCATION.
RC TISSUE=Macrophage;
RX MEDLINE=96064695; PubMed=7592832;
RA Boot R.G., Renkema G.H., Strijland A., van Zonneveld A.J.,
RA Aerts J.M.F.G.;
RT "Cloning of a cDNA encoding chitotriosidase, a human chitinase
RT produced by macrophages";
RL J. Biol. Chem. 270:26252-26256 (1995).
RN [2]
RP SEQUENCE OF 22-42 AND 178-198, FUNCTION, AND TISSUE SPECIFICITY.
RX MEDLINE=95138187; PubMed=7836450;
RA Renkema G.H., Boot R.G., Muijsers A.O., Donker-Koogman W.E.,
RA Aerts J.M.F.G.;
RT "Purification and characterization of human chitotriosidase, a novel
RT member of the chitinase family of proteins.";
RL J. Biol. Chem. 270:2198-2202 (1995).
RN [3]
RP POLYMORPHISM, AND DESCRIPTION OF ISOFORM 3.
RX MEDLINE=98421482; PubMed=9748235;
RA Boot R.G., Renkema G.H., Verhoeck M., Strijland A., Bliet J.,
RA de Meuleneester T.M.A.M.O., Mannens M.M.A.M., Aerts J.M.F.G.;
RT "The human chitotriosidase gene. Nature of inherited enzyme
RT deficiency.";
RL J. Biol. Chem. 273:25680-25685 (1998).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 22-386 IN COMPLEX WITH
RP CHITOBIOSE AND ALLOSAMIDIN.
RX MEDLINE=22095530; PubMed=11960986;
RA Fusetti F., von Moeller H., Houston D., Rozeboom H.J., Dijkstra B.W.,
RA Boot R.G., Aerts J.M.F.G., van Aalten D.M.F.;
RT "Structure of human chitotriosidase. Implications for specific
RT inhibitor design and function of mammalian chitinase-like lectins.";
RL J. Biol. Chem. 277:25537-25544 (2002).
CC -!- FUNCTION: Degrades chitin and chitotriose. May participate in the
CC defense against nematodes and other pathogens. Isoform 3 has no
CC enzymatic activity.
CC -!- CATALYTIC ACTIVITY: Hydrolysis of the 1,4-beta-linkages of N-
CC acetyl-D-glucosamine polymers of chitin.
CC -!- SUBUNIT: Monomer.
CC -!- SUBCELLULAR LOCATION: Secreted. A small proportion is lysosomal.
CC -!- ALTERNATIVE PRODUCTS:
CC Name=1;
CC IsoId=Q13231-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q13231-2; Sequence=VSP_008631, VSP_008632;
CC Name=3;
CC IsoId=Q13231-3; Sequence=VSP_008633;
CC Note=Duplication of 24 bp in exon 10 leads to the use of a
CC cryptic splice site. The normal splice site is still present but
CC not used;
CC -!- TISSUE SPECIFICITY: Detected in spleen. Secreted by cultured
CC macrophages.
CC -!- POLYMORPHISM: A 24 bp duplication in exon 10 leads to the
CC activation of an alternative splice site and the production of an
CC inactive protein. About 6% of the population are deficient for
CC CHIT1 activity, while 35% are carriers and show reduced enzyme
CC levels. People with CHIT1 deficiency appear perfectly healthy.
CC [MIM:230800] have very high plasma levels of CHIT1, and this can
CC be used as diagnostic aid and to evaluate the success of
CC treatment. Successful therapy brings the CHIT1 activity levels
CC back to normal.
CC -!- SIMILARITY: Belongs to chitinase class II (family 18 of glycosyl
CC hydrolases).
CC -!- SIMILARITY: Contains 1 chitin-binding type-2 domain.
```



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CC or send an email to licensee@isb-sib.ch).
CC -----
DR EMBL; AF026500; AAB81858.1; -.
DR FlyBase; FBgn022703; Cht1.
DR InterPro; IPR001223; Glyco_hydro_18.
DR InterPro; IPR001579; Glyco_hydro_18As.
DR Pfam; PF00704; Glyco_hydro_18; 2.
DR ProDom; PD000471; Glyco_hydro_18; 2.
DR SMART; SM00636; Glyco_18; 1.
DR PROSITE; PS01095; CHITINASE 18; 1.
KW Hydrolase; Glycosidase; Chitin degradation; Multigene family.
FT ACT_SITE 264 264 PROTON DONOR (BY SIMILARITY).
SQ SEQUENCE 508 AA; 57751 MW; 26CA23B02EFDEB97 CRC64;

Query Match 23.3%; Score 723; DB 1; Length 508;
Best Local Similarity 39.8%; Pred. No. 1.1e-32;
Matches 144; Conservative 71; Mismatches 121; Indels 26; Gaps 9;

Qy 34 RIVCVGTWSTYHK-VDPYTIETIDDPKCTHLMYGFADIKDEYKTIQVDFPYQDDNHSW 92
Dy 143 KIICFTNMYWROGGKFLPEDIDSLCTHIYGFVLSRDNLTIQ-----PHDSW 194
Qy 93 ---EKRYERPNRLKNPBLTWTISLGGNYBGS-EKYSMAANPTVROQFIQSIVLDFLQ 148
Dy 195 ADLNNKTYERIVAYRKKGAKVT--VAIGWWDGAGDKYSLVRNPARSFIRNVLDFTIE 252
Qy 149 EYKEDGDLIDWEYP-----GSLGNPKDKQNYLALVRELKDAFEHPHYLLTAAVSPGKD 203
Dy 253 EYNPDGDLIDWEYPVQVQVCKKGTAB-EKIGFSALVRELFYAFQPRGLTISAAPVFNK 311
Qy 204 KIDRAYDIKELNKLFDMMVNTVDYHGGWENFYGHNAFLYKRPDETDLHTYFNVTWH 263
Dy 312 VIDAGYEVAELSHVFTSWISVWADYHGQWDKTKGHVAPMYSHEGT-----ANFNAPFSMN 367
Qy 264 YILNAGYATRDKLNVGPFYGRAMSIDRSKLKLGDPFAKGNPPGFTSGEGVLSYIELCQ 323
Dy 368 YWISMGADRRKLNVGILYQGSFLAETTKHQLNAPTYGGEAGEATRAGFLAYVEICL 427
Qy 324 LFOKEEWHIQVEYNN-APGYNDKIWGVYDDIASICKLAFIKELGVSGVWVMSLEND 382
Dy 428 KIRHRRVNVVDTKGRIGPFAYHGQWSPDDVPMIRHKYIKAMGLGGAMIWALDLD 487
Qy 383 FK 384
Dy 488 FK 489

RESULT 5
CHIA HUMAN
ID CHIA HUMAN STANDARD; Q9ULY3; Q9ULY4; 476 AA.
AC Q9BZP6; Q86UD8; Q9ULY3; Q9ULY4;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Acidic mammalian chitinase precursor (EC 3.2.1.14) (AMCase)
DE (TSA1902).
GN CHIA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 2 AND 3).
RC TISSUE=Lung;
RA MEDLINE=2004b184; PubMed=10548734;
RX Saito K., Ozaki K., Fujiwara T., Nakamura Y., Tanigami A.;
RT "Isolation and mapping of a human lung-specific gene, TSA1902,
RT encoding a novel chitinase family member.";
RL Gene 239:325-331(1999).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1), FUNCTION, AND TISSUE SPECIFICITY.
RC TISSUE=Lung, and Stomach;
RX MEDLINE=21125893; PubMed=11085997;

RA Boot R.G., Blommaert E.F.C., Swart E., Chauharali-van der Vlugt K.,
RA Bijl N., Moe C., Place A., Aerts J.M.F.G.;
RT "Identification of a novel acidic mammalian chitinase distinct from
RT chitotriosidase.";
RL J. Biol. Chem. 276:6770-6778(2001).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jorda H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Degrades chitin and chitotriose. May participate in the
CC defense against nematodes and other pathogens.
CC -!- CATALYTIC ACTIVITY: Hydrolysis of the 1,4-beta-linkages of N-
CC acetyl-D-glucosamine polymers of chitin.
CC -!- SUBCELLULAR LOCATION: Secreted (Probable). Isoform 2 and isoform 3
CC lack the signal sequence and are cytoplasmic.
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=3;
CC Name=1;
CC IsoId=Q9BZP6-1; Sequence=Displayed;
CC Name=2; Synonyms=TSA1902-L;
CC IsoId=Q9BZP6-2; Sequence=VSP_008635;
CC Name=3; Synonyms=TSA1902-S;
CC IsoId=Q9BZP6-3; Sequence=VSP_008634;
CC -!- TISSUE SPECIFICITY: Highly expressed in stomach. Detected at lower
CC levels in lung.
CC -!- SIMILARITY: Belongs to chitinase class II (family 18 of glycosyl
CC hydrolases).
CC -!- SIMILARITY: Contains 1 chitin-binding type-2 domain.
CC -----
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CC -----
CC EMBL; AB025008; BAA86980.1; -.
CC EMBL; AB025009; BAA86981.1; -.
CC EMBL; AF290004; AAG60019.1; -.
CC EMBL; BC047336; AAH47336.1; ALT_INIT.
CC MIM; 605080; -.
CC GO; GO:0005737; Cytoplasm; NAS.
CC GO; GO:0004568; P:chitinase activity; NAS.
CC GO; GO:0006030; P:chitin metabolism; NAS.
CC InterPro; IPR002557; Chitin bind PerA.
CC InterPro; IPR001223; Glyco_hydro_18.
CC InterPro; IPR001579; Glyco_hydro_18As.
CC Pfam; PF01607; CSM_14; 1.
CC Pfam; PF00704; Glyco_hydro_18; 1.
CC ProDom; PD000471; Glyco_hydro_18; 1.
CC SMART; SM00494; ChtBD2; 1.
CC SMART; SM00636; Glyco_18; 1.
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[illegible]


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DR PTR; S57197; S57197.
DR InterPro; IPR001223; Glyco_hydro_18.
DR InterPro; IPR001579; Glyco_hydro_18AS.
DR Pfam; PF000471; Glyco_hydro_18; 1.
DR ProDom; PD000471; Glyco_hydro_18; 1.
DR SMART; SM00636; Glyco_18; 1.
DR PROSITE; PS01095; CHITINASE_18; FALSE_NEG.
KW Glycoprotein; Fertilization; Signal.
FT SIGNAL 1 1
FT CHAIN 41 18
FT CATH 19 537
FT CARBOHYD 399 399
FT SEQUENCE 537 AA; 59617 MW; CFDCB6F0212D791 CRC64;
SQ SEQUENCE 537 AA; 59617 MW; CFDCB6F0212D791 CRC64;

Query Match 22.1%; Score 685.5; DB 1; Length 537;
Best Local Similarity 33.3%; Pred. No. 1.3e-30;
Matches 173; Conservative 95; Mismatches 183; Indels 69; Gaps 19

Qy 10 INACIGLMNASTIKRDHNDYKKNPMRIVCVGTWVSVKHKVDPIYT--EDIDPKCTHLMYG 67
Db 1 LLLCVGLL---LVLRKHDAAH--KLVCYFTNMA-FSRPGPASILPRDLDPFLCTLHVAFA 54
Qy 68 EAKIDEVKYTIQVPDPYODDNHNSKEKGVERFNRLKKNPELTMTISLGGMVEGSEKXS 127
Db 55 FASMSNQ--IVPKDP-QD-----EKILYPEFKLKERNRGLKTLISGGWNFGTVRAFT 105
Qy 128 DAAANPTVQQFIQSVLDFLOEYFGDGLDDWEYPFSRSLGNPKIDIKONTYLALVRILKOAF 187
Db 106 TMLSTFSNRERFVSSVIALLRTHRGFDGLDLFFLYPLGR-GSPARDRTVFVLEELLQAF 164
Qy 188 EPHG-----YLLTAAVSPGKKIDRAYDIKEINKLFDMNVMTYDYHGWFNFYGHNA 240
Db 165 KNEAQLTMRPLLGAAYSGDPHVYQKAYEARLLGRLLDFISVLSYDLHGSEKVTGHS 224
Qy 241 PLYKRPFDELDHTFVNNTWHYYLNGATRDKLVMGVPPYGRANSIEDRSKLKLGPA 300
Db 225 PLFSPGDPK-----SSAYAMVWRQGVPEPKLLMGLPTYGRTFHLLKASQNELRAQA 278
Qy 301 KGMSPPGFISGEYGVLSELQCFQKEWHIQDEYNAPYGVNDKIWWGVDDLASISC 360
Db 279 VGPASGKTKXAGFLAYEICCFVRACKEWINDQY-VPYAFKGEWVGVDLAISFGY 336
Qy 361 KLAFKELGVSGVMYSLENDDFKGH-CGP-KNFLANKVNMMINGDKNSFCILGPSTT 418
Db 337 KAFFIKREHFGGAMVWLDDLDFRGYFCGTGFPFLVHTLNLLNWDEFSS----- 386
Qy 419 TTPT-----TTTTTTTTPPTPSPTTPTTPTSPPTP-----TTTTPTPTTPTPTPT 466
Db 387 TSPKFWFSTAYNSSRIGEPMTTRDTLTLGLTFPGGEAVATETHRKSETMTITPKGE 446
Qy 467 TTPT-T-P-----TPATTTPGP-----TTTEHTSETP 494
Db 447 IATPTPTPSFGHHTAAPEGKTSPGKPLTTVCHLAVSP 486

RESULT 9
OGP_SHEEP STANDARD; PRS; 539 AA.
AC Q28542; Q28543;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Oviduct-specific glycoprotein precursor (Oviductal glycoprotein)
DE (Oviductin) (estrogen-dependent oviduct protein) (Estrus-associated oviductal glycoprotein) (OEGP).
DE OVGP1 OR OGP.
GN Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_Taxid=9940;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 22-39.

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DR SMART, SM00636; Glyco_18; 1.  
DR PROSITE; PS01095; CHITINASE_18; FALSE NEG.  
KW Glycoprotein; Fertilization; Repeat; Signal.  
FT SIGNAL 1 21 POTENTIAL.  
FT CHAIN 22 721 OVIDUCT-SPECIFIC GLYCOPROTEIN.  
FT DOMAIN 486 632 [TAP]-G-[IV].  
FT CARBOHYD 402 402 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 442 442 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 469 469 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 721 AA; 78807 MW; 37246C8F01665652 CRC64;  
  
Query Match 21.9%; Score 680; DB 1; Length 721;  
Best Local Similarity 33.7%; Pred. No. 3.6e-30;  
Matches 175; Conservative 79; Mismatches 184; Indels 82; Gaps 16;  
  
QY 34 RIVCVGTWVYHKVDYTI--EDIDPKCTHLMYGFADKIDYKTYIQVDPDQDNHNS 91  
DB 23 KLVCYFTNWA--HSRPGPASIMPHDLDPFLCTHLIFAPASNNQI---VAKNLQDENVL- 77  
QY 92 WEKGYERFNNLRKKNPELTMTISLGGWYEGSEKYSDMAANPTYRQOFIOSVLDLQEQYK 151  
DB 78 -----YFEFNKLKERNRELKTLISIGGNWFGTGRFTAMLTSLANREKFDVSIPLRIHG 132  
QY 152 FDGLDLQWYVPGSLGNPKIDKONYALVRELKDAPEPHG-----YLLTAAVSPGKDK 204  
DB 133 FDGLDLFLFLPGLR--GSPPHDRWNFLFLIELQAPAFERBALLTQHPRLLLSAAVSGIPSI 191  
QY 205 IDRAYDIKELNKLFDWNNVMTYDHYGGWENFYGNAPLYKRPDETDELHTYFNNVNTMYH 264  
DB 192 IHTSYDALLGRRDLDFNLVSLDHLGWSWEXFTGHSPLFLSPEDSK-----SSAYAMNY 245  
QY 265 YLNNGATRDKLVMGVPPYGRAMSTEDRSKULGDPKMGSPPFISGEEGVLSYIELCOL 324  
DB 246 WRKLGTPADKLIMFPYTYGRNLYLLKESKNGLOQTASMGPSAPGKYTKAQGLAYEVCSP 305  
QY 325 FQKEWHIQDYVYNAQYNDKILWGYDDLASLKLFLKELGVGMVWNSLENDFFX 384  
DB 306 VQRAKKE--WIDYQVYPAFKGEWLGYDDTISFYKAMYKREHFGGANVWTLDMDDVR 363  
QY 385 G-HCG-PKNPLNKNVNMINGDEKNSPECILGPSTTTPTP----- 422  
DB 364 GTFCNGNPPFLVHLINELLVQTESN-----TLPQFQWFTSSVNASGPGSENTAL 413  
QY 423 ----TTTTPTPTTTTTPSPPTP-----TTTPS--PTTPTTTPSPPTTPTTPTTPTTPT 469  
DB 414 TEVLTITTIKILPGGEMATEVHRYENMTVPDSCGVTFPGTASPKHATVPENNTWA 473  
QY 470 PTTPTP-----APTTPSPPTT---EHTSETPKYTYV 500  
DB 474 AEAKTMSTLDPFSKTTTGVSKTITGSKTTTGVSKTITGV 513  
  
RESULT 13  
ID_OGP HUMAN STANDARD; PRT; 678 AA.  
AC Q12889; Q15841;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Oviduct-specific glycoprotein precursor (Oviductal glycoprotein)  
DE (Oviductin) [Estrogen-dependent oviduct protein] (Mucin 9).  
GN OVGPI OR OGP OR MUC9.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Oviduct;  
RX MEDLINE=95119256; PubMed=7819450;  
RA Arias E.B., Verhage H.G., Jaffe R.C.;  
RT "Complementary deoxyribonucleic acid cloning and molecular
```

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RT RT  
RT glycoprotein.";  
RL Biol. Reprcd. 51:685-694(1994).  
RN [2]  
RP SEQUENCE FROM N.A., AND VARIANT GLN-676.  
RA Jaffe R.C.;  
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RA Coville G.;  
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: Binds to oocyte zona pellucida in vivo. May play a role  
CC in the fertilization process and/or early embryonic development.  
CC -!- SUBCELLULAR LOCATION: Secretory granules.  
CC -!- TISSUE SPECIFICITY: Oviduct.  
CC -!- SIMILARITY: Belongs to family 18 of glycosyl hydrolases.  
CC  
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CC  
CC EMBL; U09550; A2A86946.1; -  
CC EMBL; U58010; AAB04126.1; -  
DR EMBL; U58001; AAB04126.1; JOINED.  
DR EMBL; U58002; AAB04126.1; JOINED.  
DR EMBL; U58003; AAB04126.1; JOINED.  
DR EMBL; U58004; AAB04126.1; JOINED.  
DR EMBL; U58005; AAB04126.1; JOINED.  
DR EMBL; U58006; AAB04126.1; JOINED.  
DR EMBL; U58007; AAB04126.1; JOINED.  
DR EMBL; U58008; AAB04126.1; JOINED.  
DR EMBL; U58009; AAB04126.1; JOINED.  
DR EMBL; AL390195; CAC36039.1; -  
DR Genew; HGNC:8524; OVGPI.  
DR MIM; 603578; -  
DR GO; GO:0007565; P:pregnancy; TAS.  
DR InterPro; IPR001223; Glyco_hydro_18.  
DR InterPro; IPR001579; Glyco_hydro_18AS.  
DR Pfam; PF00704; Glyco_hydro_18; 1.  
DR ProDom; PD000471; Glyco_hydro_18; 1.  
DR SMART; SM00636; Glyco_18; 1.  
DR PROSITE; PS01095; CHITINASE_18; FALSE NEG.  
KW Glycoprotein; Fertilization; Signal; Polymorphism.  
FT SIGNAL 1 21 BY SIMILARITY:  
FT CHAIN 22 678 OVIDUCT-SPECIFIC GLYCOPROTEIN.  
FT CARBOHYD 402 402 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 441 441 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 580 580 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 596 596 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 648 648 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT VARIANT 676 676 E -> Q (in dbSNP:7825).  
FT CONFLICT 477 477 M -> T (IN REF. 2).  
FT CONFLICT 511 511 S -> P (IN REF. 2).  
FT CONFLICT 514 514 Y -> H (IN REF. 2).  
SQ SEQUENCE 678 AA; 75421 MW; 245F2CEDC92768B CRC64;  
  
Query Match 21.5%; Score 668; DB 1; Length 678;  
Best Local Similarity 33.1%; Pred. No. 1.5e-29;  
Matches 176; Conservative 91; Mismatches 192; Indels 72; Gaps 19;  
  
QY 10 IMACIGLMMASIKRDHNDYKPMRIVCVGTWVYHKVDYTI--EDIDPKCTHLMYK 67  
DB 4 LLLWGLV--LVLKHHDDGAH--KLVCYFTNWA--HSRPGPASILPHDLDPFLCTHLIFA 57  
QY 68 FAKIDBYKTYIQVDPDQDNHNSKGYERFNNLRKKNPELTMTISLGGWYEGSEKYS 127  
DB 58 FASMMNNQI---VAKDLQD-----EKILYFENFKERNRELKTLISIGGNWFGTGRFT 108
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QY 128 DMAANPTYRQFIQSVDLFLQYKFDGLDLDWEYPSGRLGNPKIDKONYALVRELKDAF 187
DB 109 TMLSTPEANREKFIASVLSLRTHDFGLDFFLYPGLR-GSPWHDRAWTFLEELFAF 167
QY 188 EPHG-----YLTAASVSCCKIDIRAYDIKEINLKLFDWNTVMTYHGCWENFYCHNA 240
DB 168 RKEALLTWPRLLLSAAVSGVPHIVQTSYDVRFGLRLDFFINLSYDLHGSWERFTGHNS 227
QY 241 PLYKRPDETDELHYTFVNVNTHYLLNNGATRDKLVMGVFFYGRANSIEDRSKLKLGDDPA 300
DB 228 PLFSLPBDPK-----SSAYAMNWRKLGAPSEKLMGIFTYGRTPFLKASKNGLOARA 281
QY 301 KGMSPPGFISGEGVLGYIELCOLF--QKBEWHIQYDEYNNAPYGVNDKIWGYDDLASI 358
DB 282 IGPASPGKYKQEGFLAYFICFSVMGAKKH-----IDYQVVPYANKGKWWGVYDAISF 337
QY 359 SKLAFKLKELGVSGVMVWSLENDPKG-HCGP-KNPLINKVHNMINGDEKNSFECILGPS 416
DB 338 SYKAWFIRREHFGGAMVWTLDDVDRGTFCGTGPFPLVYVLDILVRAEFS-----S 389
QY 417 TTTPT--PTTPTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPT 466
DB 390 TSLPQFWLSSAVNSSTDPERLAVTTATWTDKILPGGEAGVTEIHGKCNMTITPRGT 449
QY 467 TPTPTPT-----PAPTSTPPTTTEHTGETP--KYTTYVDGH 503
DB 450 TVTPTKTVSLGKTVLGEKTEITGATWTSVGHQSWTPEKALTPV-GH 499

RESULT 14
C3L1_HUMAN
ID C3L1_HUMAN STANDARD; PRT; 383 AA.
AC P36222; P30923;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Chitinase-3 like protein 1 precursor (Cartilage glycoprotein-39) (GP-39) (39 kDa synovial protein) (YKL-40).
GN CH3L1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Cartilage;
RX MEDLINE=94064658; PubMed=8245017;
RA Hakala B.E.; White C.; Recklies A.D.;
RT "Human cartilage gp-39, a major secretory product of articular chondrocytes and synovial cells, is a mammalian member of a chitinase protein family.";
RL J. Biol. Chem. 268:25803-25810(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=97386591; PubMed=9244440;
RA Rehli M.; Krause S.W.; Andresen R.;
RT "Molecular characterization of the gene for human cartilage gp-39 (CH3L1), a member of the chitinase protein family and marker for late stages of macrophage differentiation.";
RL Genomics 43:221-225(1997).
RN [3]
RP SEQUENCE OF 22-45.
RX MEDLINE=90328983; PubMed=2375755;
RA Nytkos P.; Golds E.E.;
RT "Human synovial cells secrete a 39 kDa protein similar to a bovine mammary protein expressed during the non-lactating period.";
RL Biochem. J. 269:265-268(1990).
CC -!- FUNCTION: May play an important role in the capacity of cells to respond to and cope with changes in their environment.
CC -!- SUBCELLULAR LOCATION: Extracellular.
CC -!- TISSUE SPECIFICITY: Present in articular chondrocytes, synovial cells as well as in liver. Undetectable in muscle tissues, lung,
```

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CC pancreas, mononuclear cells, or fibroblasts.
CC -!- PTM: Glycosylated.
CC -!- SIMILARITY: Belongs to family 18 of glycosyl hydrolases.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M80927; AAA16074.1; -.
CC EMBL; Y08374; CAA69661.1; -.
CC EMBL; Y08375; CAA69661.1; JOINED.
CC EMBL; Y08376; CAA69661.1; JOINED.
CC EMBL; Y08377; CAA69661.1; JOINED.
CC EMBL; Y08378; CAA69661.1; JOINED.
CC FIR; A49562; A49562.
CC PDB; 1LA7; 10-APR-02.
CC Genew; HGNC:1932; CH3L1.
CC MIM; 601525; -.
CC GO; GO:0005578; C:extracellular matrix; TAS.
CC GO; GO:0005615; C:extracellular space; TAS.
CC GO; GO:0005201; F:extracellular matrix structural constituent; TAS.
CC InterPro; IPR001223; Glyco_hydro_18.
CC InterPro; IPR001579; Glyco_hydro_18AS.
CC Pfam; PF00704; Glyco_hydro_18; 1.
CC ProDom; PD000471; Glyco_hydro_18; 1.
CC SMART; SM00636; Glyco_18; 1.
CC PROSITE; PS01095; CHITINASE_18; FALSE_NEG.
KW Glycoprotein; Signal; 3D-structure.
FT SIGNAL 1 21 CHITINASE-3 LIKE PROTEIN 1.
FT CHAIN 22 383 N-LINKED (GLUCNAC...)(POTENTIAL).
FT CARBOHYD 60 60 76ADD8298BEECD1 CRC64;
SQ SEQUENCE 383 AA; 42613 MW; 76ADD8298BEECD1 CRC64;

Query Match 21.3%; Score 662; DB 1; Length 383;
Best Local Similarity 34.9%; Pred. No. 1.7e-29;
Matches 144; Conservative 81; Mismatches 136; Indels 52; Gaps 12;

QY 2 KTIYALISIMAGITGLMNASIKRDHNDYKSNPRIVCYVGTWTSVHKVPYTTIED-IDPFK 60
DB 7 QTGFVVLVLQCC-----SAYKLVCYITSWSQYREGDSCFPDLDRLF 50
QY 61 CTHLMYGFPAKIDYKTYIQVDPYQDNNHNSKEKG---YERFNNLRKNBELTMTWISLG 117
DB 51 CTHIISFANI-----SNDHDTWEWNDVTLYGLMNTLKNRPNLKLTSVSG 97
QY 118 GWYEGSEKSDMAANPTYRQFIQSVDLFLQYKFDGLDLDWEYPSGRLGNPKIDKONYL 177
DB 98 GWNFGSQRFSKIASNTQSRRTFKSVPPFLRTHGPDGLAWLDPGRR-----DRQHFT 151
QY 178 ALVRELKDAF---EP--HGVLTTAAVSPGKDKIDRAYDIKEINLKLFDWNTVMTYDHGG 231
DB 152 TLIKEMKAEFIKAEQPKQLLSAALSAGKTISSYDIKISQHLDFISIMTYDFHGA 211
QY 232 WENFYGHNAFLYKRPDETDELHYTFVNVNTHYLLNNGATRDKLVMGVFFYGRANSIEDR 291
DB 212 WRGTTGHSPLEF--RGQEDASDPRESNTDVAVGVMRLGAPASKLVNGIPTFGKSFSLAS- 269
QY 292 SKLKGDPKAGMSPPGFISSGEGVLGYIELCOLFQKEEWHIQYDEYNNAPYGVNDKIWVG 351
DB 270 SETGVGAPISGGPIGPRFTKEAGTLLAYEICDFLRGATVHRTLGQ--QVFPATKGNQWVG 327
QY 352 YDDLASISCKLAFKLKELGVSGVMVWSLENDPKG-HCGP--KNPLINKVHNM 401
DB 328 YDDQESVKSKVQLKDRQLAGAMVWALDDDFQGSFGQDLRPLPLTNALKDAL 380

RESULT 15
OGP_PAPAN
ID OGP_PAPAN STANDARD; PRT; 623 AA.
```


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OM protein - protein search, using sw model

Run on: March 22, 2004, 06:39:53 ; Search time 111.679 Seconds
(without alignments)
1568.003 Million cell updates/sec

Title: US-09-662-293-15
Perfect score: 3107
Sequence: 1 MKTIYALLSIACIGLMNAS.....IMPCPPQTWCQEKLCIGCE 555

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: SP archaea.*
- 2: SP bacteria.*
- 3: SP fungi.*
- 4: SP human.*
- 5: SP invertebrate.*
- 6: SP mammal.*
- 7: SP mhc.*
- 8: SP organelle.*
- 9: SP phage.*
- 10: SP plant.*
- 11: SP rodent.*
- 12: SP virus.*
- 13: SP vertebrate.*
- 14: SP unclassified.*
- 15: SP rivirus.*
- 16: SP bacteriap.*
- 17: SP archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3107	100.0	555	5	Q9U6R7 dermatophag
2	1008.5	32.5	525	5	Q44079 anopheles g
3	942	30.3	431	5	Q151SH5 araneus ven
4	869	28.0	1635	5	Q17412 aedes aegyp
5	854.5	27.5	4498	5	Q9W223 drosophila
6	847	27.3	544	5	Q9GQC4 bombyx mori
7	842	27.1	2838	5	Q9MP05 tenebrio mo
8	839	27.0	566	5	Q9WR52 bombyx mori
9	837.5	27.0	467	5	Q15993 penaeus jap
10	837.5	27.0	543	5	Q9GR93 bombyx mori
11	837.5	27.0	543	5	Q9GV05 bombyx mori
12	837.5	27.0	565	5	P90710 bombyx mori
13	837.5	27.0	595	5	Q9VFR3 drosophila
14	832	26.8	460	5	Q9W2M7 drosophila
15	831.5	26.8	467	5	Q9ITU3 penaeus van
16	829.5	26.7	565	5	Q9GP59 bombyx mand

17	823.5	26.5	557	5	Q8WTK0	Q8ntk0 choristoneu
18	823	26.5	488	13	Q9OW34	Q9ow34 bufo japoni
19	814.5	26.2	552	5	Q9GV44	Q9gv44 spodoptera
20	810	26.1	574	5	Q17411	Q17411 aedes aegyp
21	802	25.8	483	5	Q23737	Q23737 chelonus sp
22	798	25.7	572	5	Q26042	Q26042 penaeus jap
23	790	25.4	620	5	Q9Y0D4	Q9y0d4 penaeus mon
24	787	25.3	553	5	P91731	P91731 hyphatria
25	780	25.1	470	13	Q803B7	Q803b7 brachydanio
26	762.5	24.5	474	5	Q86LZ2	Q86l22 lutzomyia 1
27	754	24.3	500	13	Q7ZV48	Q7zv48 brachydanio
28	738	23.8	466	4	Q13231	Q13231 homo sapien
29	736.5	23.7	473	11	Q99PH2	Q99ph2 mus musculu
30	734.5	23.6	472	11	Q9JLN1	Q9jln1 mus musculu
31	734.5	23.6	473	11	Q9D803	Q9d803 mus musculu
32	733	23.6	482	13	Q8AV87	Q8av87 gallus gall
33	732.5	23.6	387	4	Q9H3V8	Q9h3v8 homo sapien
34	731.5	23.5	472	6	Q9SM17	Q9sm17 bos taurus
35	723.5	23.3	688	5	Q8MS85	Q8ms85 drosophila
36	722.5	23.3	1013	5	Q96OM0	Q96om0 drosophila
37	717	23.1	527	5	P91773	P91773 penaeus jap
38	716	23.0	460	5	Q8WS95	Q8ws95 glossina mo
39	710	22.9	484	5	Q9W092	Q9w092 drosophila
40	708.5	22.8	476	4	Q9BZP6	Q9b2p6 homo sapien
41	703	22.6	929	5	Q8MY79	Q8my79 haemaphysal
42	702.5	22.6	983	5	Q9VZV2	Q9vzv2 drosophila
43	691	22.2	462	5	Q9W2M6	Q9w2m6 drosophila
44	687	22.1	381	11	Q99J84	Q99j84 mus musculu
45	687	22.1	389	11	Q9BKL8	Q9bkl8 mus musculu

ALIGNMENTS

RESULT 1

Q9U6R7	PRELIMINARY;	PRT;	555 AA.
ID	Q9U6R7		
AC	Q9U6R7;		
DT	01-MAY-2000 (TREMBLrel. 13, Created)		
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)		
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)		
DE	98kDa HDM allergen.		
OS	Dermatophagoides farinae (House-dust mite).		
OC	Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;		
OC	Acariiformes; Sarcoptiformes; Astigmata; Psoroptidia; Analgoidea;		
OC	Pyroglyphidae; Dermatophagoides.		
OX	NCBI_TaxID=6954;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Weber E.R., Hunter S., Stedman K., McCall C.;		
RT	"Cloning and Characterization of a 98 kDa Allergen from		
RL	Dermatophagoides farinae."		
RL	Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF18772; AAD52672.1;		
DR	GO; GO:0005576; C:extracellular; IEA.		
DR	GO; GO:0008061; F:chitin binding; IEA.		
DR	GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.		
DR	GO; GO:0005975; P:carbohydrate metabolism; IEA.		
DR	GO; GO:0006030; P:chitin metabolism; IEA.		
DR	InterPro; IPR001223; Chitin bind PefA.		
DR	InterPro; IPR001223; Glyco hydro 18.		
DR	InterPro; IPR001579; Glyco hydro 18AS.		
DR	Pfam; PF00704; Glyco hydro 18; 1_18AS.		
DR	ProDom; PD000471; Glyco hydro 18; 1.		
DR	SMART; SM00494; ChtBD2; 1.		
DR	SMART; SM00636; Glyco 18; 1.		
DR	PROSITE; PS01095; CHITINASE_18; 1.		
KW	Glycosidase; Hydrolase.		
SQ	SEQUENCE 555 AA; 63238 MW; 0E4564A1A459B30B CRC64;		

Query Match 100.0%; Score 3107; DB 5; Length 555;
Best Local Similarity 100.0%; Pred. No. 2.9e-186;
Matches 555; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


```
QY 1 MKTIYAILSIMACIGLNASIKRDNDYSKNPMRIVCVGWSVYHKVDPTTIEDIDPFK 60
DB 1 MKTIYAILSIMACIGLNASIKRDNDYSKNPMRIVCVGWSVYHKVDPTTIEDIDPFK 60
QY 61 CTHLMYGAFAKIDYKTYIQVDFPYQDDNHNNSWEKRGYERFNNRLKNPELTMTISLGGWY 120
DB 61 CTHLMYGAFAKIDYKTYIQVDFPYQDDNHNNSWEKRGYERFNNRLKNPELTMTISLGGWY 120
QY 121 EGSEKYSMAANPTVROQFIQSVDLFOEYKFDGLDWEYFSGRLGNPKDKONYLALV 180
DB 121 EGSEKYSMAANPTVROQFIQSVDLFOEYKFDGLDWEYFSGRLGNPKDKONYLALV 180
QY 181 RELKDAFPHGVLTAAYSPGKDKIDRAYDIKELNKLFDWNNVMTYDYHGGWENFYGHNA 240
DB 181 RELKDAFPHGVLTAAYSPGKDKIDRAYDIKELNKLFDWNNVMTYDYHGGWENFYGHNA 240
QY 241 PLYKRPDTELTHTYFNNVNTMYYLNGNATRDKLVMGVPPFYGRAWSIEDRSKLKLGDP 300
DB 241 PLYKRPDTELTHTYFNNVNTMYYLNGNATRDKLVMGVPPFYGRAWSIEDRSKLKLGDP 300
QY 301 KMSPPGFSISGEGVLSYIELCOLFQKEWHIOYDEYNAPYGYNDKIWVGYYDDLASISC 360
DB 301 KMSPPGFSISGEGVLSYIELCOLFQKEWHIOYDEYNAPYGYNDKIWVGYYDDLASISC 360
QY 361 KLAFLKELGVSGVMVWSLENDDFKHCGCPKPLNKNVNMINGDEKNSFECILGPSTTTP 420
DB 361 KLAFLKELGVSGVMVWSLENDDFKHCGCPKPLNKNVNMINGDEKNSFECILGPSTTTP 420
QY 421 TPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPT 480
DB 421 TPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPT 480
QY 481 TSPPTTHTSTPKYTYVVDGHLIKCYKEGDIHPHTNIHKYLVCYFVNGGWWHIMPCP 540
DB 481 TSPPTTHTSTPKYTYVVDGHLIKCYKEGDIHPHTNIHKYLVCYFVNGGWWHIMPCP 540
QY 541 PGTWCQKLCIG 555
DB 541 PGTWCQKLCIG 555

RESULT 2
O44079 PRELIMINARY; PRT; 525 AA.
ID O44079
AC O44079;
DT 01-JUN-1998 (TREMELrel. 06, Created)
DT 01-JUN-1998 (TREMELrel. 06, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Chitinase.
GN AGChi-1.
OS Anopheles gambiae (African malaria mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX NCBI_TaxID=7165;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Gut;
RA MEDLINE=98030563; PubMed=9360958;
RT "Characterization of a novel gut-specific chitinase gene from the
RT human malaria vector Anopheles gambiae."
RL J. Biol. Chem. 272:28895-28900(1997).
DR EMBL; AF008575; AAB87764.1; -.
DR PIR; T44445; T44445
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008061; F:chitin binding; IEA.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0006030; P:chitin metabolism; IEA.
DR InterPro; IPR002557; Chitin_bind.Pera.
DR InterPro; IPR001223; Glyco_hydro.18.
DR InterPro; IPR001579; Glyco_hydro.18AS.
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DR Pfam; PF01607; CBM_14; 1.
DR Pfam; PF00704; Glyco_hydro.18; 1.
DR ProDom; PD000471; Glyco_hydro.18; 1.
DR SMART; SM00494; ChtB2; 1.
DR SMART; SM00636; Glyco.18; 1.
DR PROSITE; PS01095; CHITINASE_18; 1.
KW Glycosidase; Hydrolase.
SQ SEQUENCE 525 AA; 57211 MW; 3234360EFFF36165 CRC64;

Query Match 32.5%; Score 1008.5; DB 5; Length 525;
Best Local Similarity 38.4%; Pred. No. 4e-55;
Matches 211; Conservative 93; Mismatches 187; Indels 59; Gaps 13;

QY 8 LSIMACIGLNASIKRD-HNDYSKNPMRIVCVGWSVYHKVD-PYTIEDIDPFKCTHLM 65
DB 5 VGVILVAVAAAFAPAEHPKAASAEKKVCVGVGWAVTRPGNGRYDIHIDPSLCTHLM 64
QY 66 YGPAKIDEXYKTYIQVDFPYQDDNHNNSWEKRGYERFNNRLKNPELTMTISLGGWYSGSK 125
DB 65 YGFFGINE-DATVRIIDPYLDLEEN-WGRGHIKRFVGLXNVGPGKTLAAIGWNEGSK 122
QY 126 YSDMAANPTVROQFIQSVDLFOEYKFDGLDWEYFSGRLGNPKDKONYLALVRELKD 185
DB 123 FSAASAAGELRKEFIKDCVAFQORHGFDGIDLWYEPQORDGNPLIDRDNHAQLVEEMRE 182
QY 186 APEPHGVLLTAAYSPGKDKIDRAYDIKELNKLFDWNNVMTYDYHGGWENFYGHNAPLYKR 245
DB 183 EPHYGLLLTAAYSAVSEFSAVSVDIPRISKGFHLNVMVYDMHGAWSYCGINAPLYRG 242
QY 246 PDTELTHTYFNNVNTMYYLNGNATRDKLVMGVPPFYGRAWSIEDRSKLKLGDPKGMSP 305
DB 243 SADTTDLRGQINVASIHFWLAQCGCTGRKLVIGIPLYGRNFTLASAANTQIGAPTGGGT 302
QY 306 PGFISGEGVLSYIELCOLFQKEWHIOYDEYNAPYGYNDKIWVGYYDDLASISCKLAF 365
DB 303 VGYTRPGVMGVNEFCLEATEWDLRWSEQQVYAVNNQWVGYYDDLRSVQLKVYL 362
QY 366 KELGVSGVMVWSLENDDFKHCG-CPKNPLNKNVNMINGDEKNSFECILGPSTTPTTPT 424
DB 363 LDQGLGAMVWSLETDGFLGCGGGRYPLMHETIRSLVNGGT-----PSTTTMPPSV 413
QY 425 TPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPT 484
DB 414 APPT-----STVAPGTTTTTPTGANFGTTQPPT--SDAPNHTTTSTTTEGNGPTTRPPSG 466
QY 485 TTTEHTSETPKYTYVVDGHLIKCY--KEGDIHPHTNIHKYLVC-----EFVNGGWWH 535
DB 467 -----DG-----PCAGRGYGVHPHTNCARYICLTADTYVEFT----- 500
QY 536 IMPCPGTIW 545
DB 501 ---CPFGTLF 507

RESULT 3
Q8ISH5 PRELIMINARY; PRT; 431 AA.
ID Q8ISH5
AC Q8ISH5;
DT 01-MAR-2003 (TREMELrel. 23, Created)
DT 01-MAR-2003 (TREMELrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Chitinase.
OS Araneus ventricosus.
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
OC Araneomorphae; Entelegynae; Araneioidea; Araneidae; Araneus.
OX NCBI_TaxID=182803;
RN [1]
RP SEQUENCE FROM N.A.
RA Han J.H., Kim S.R., Sohn H.D., Jin B.R.;
RT "Molecular cloning of a cDNA encoding the chitinase from the spider,
RT Araneus ventricosus."
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AV120879; AAN39100.1; -.
```



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Db 2499 VLDGSTWTLKPHDSW 2513
      Q8WR52 PRELIMINARY; PRT; 566 AA.
AC Q8WR52;
DT 01-MAR-2002 (TremBLrel. 20, Created)
DT 01-MAR-2002 (TremBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Chitinase precursor (EC 3.2.1.14).
GN CHIB4.
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
OC Bombycidae; Bombyx.
OX NCBI_TaxID=7091;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Kinshu x Shoua; TISSUE=Integument;
RA Abdel-Banat B.M.A., Koga D.;
RT "Alternative mRNA splicing generates heterogeneity within Bombyx mori
RL gene for chitinase.";
DR EMBL; AF455139; AAL51080.1;
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008061; F:chitin binding; IEA.
DR GO; GO:0008843; F:endochitinase activity; IEA.
DR GO; GO:0016798; F:hydrolyase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0006030; P:chitin metabolism; IEA.
DR InterPro; IPR002557; Chitin_bind_PeR.
DR InterPro; IPR001223; Glyco_hydro_18.
DR InterPro; IPR001579; Glyco_hydro_18AS.
DR Pfam; PF01607; CBM 14; 1.
DR Pfam; PF00704; Glyco_hydro_18; 1.
DR ProDom; PD000471; Glyco_hydro_18; 1.
DR SMART; SM00494; ChitBD2; 1.
DR SMART; SM00636; Glyco_18; 1.
DR PROSITE; PS01095; CHITINASE 18; 1.
KW Signal; Hydrolase; Glycosidase.
FT SIGNAL 21 POTENTIAL.
FT CHAIN 22 566 CHITINASE.
SQ SEQUENCE 566 AA; 63465 MW; 43FC717B3F6917D0 CRC64;

Query Match 27.0%; Score 839; DB 5; Length 566;
Best Local Similarity 35.9%; Pred. No. 1.7e-44;
Matches 207; Conservative 78; Mismatches 209; Indels 82; Gaps 20;

Qy 1 MKTIYAILSIMA-CIGLMNASIKRDNDYSKNPRLVYCVGTWTSYHK-VDPYTIEDIDP 58
Db 1 MEAIFATLAVLASCAALVQCADSR-----ARIVCFNSNVAVYRPGVGRYGIEDIPV 51

Qy 59 FKCTHLMYGFAXIDYKTIQVDFPYQDNNHNSKEKGYERFNLRKNPELTMTISLGG 118
Db 52 DLCTHLYSFGIVTEKESSEVLIDPELD-----VDKSGFRNFTLSRSHKPGKFMVAVGG 106

Qy 119 WYEGSEKYSDMAANTYRQQTQSVDLQELQYKPGDLIDWEYPGSR-LGNPKIDKONYL 177
Db 107 WAEGSKSHMVAQKSTMSFIRSVDLKKYDFGLDLIDWEYFGAARGSGSPDKXFL 166

Qy 178 ALVRELKDAF--EPHYGLTAAVSPGKIDRAYDIKELNKLFDMMNMTYDYHGGWENF 235
Db 167 YFVQELKGAIFRAGRGWELTAAPLANFLRMGSHVPELQCELDIAHVMYSLRGNWAGF 226

Qy 236 YGHNAPLYKRPDETHLYFNNTMTMYLNNAGTRDKLVMGVFPFYGRANSIED----- 290
Db 227 ADVHSPLYKRPDH-QWAVEKLNVDNLWEKGCPTNKLVVGIPFYGRSFTLSAGNNNY 285

Qy 291 -----RSKLKGLDPAKGMSPGFTSGEEGLVSYELCOLFQKE--EWHIQYDEYNAPY 342
Db 286 GLGTVINKEAGGDPAPYTNATGF-----WAYVEICTEVDADGSGTKWDEFGKCPY 338
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Qy 343 GYNDKIMVGYDDIASISCKLAPLKLGVSGVNVWSLENDDFKGGHCPKPKNPLLNKVNMIN 402
Db 339 AYKGTQWGVYEDPRSVIEIKANWIKKGYLGAMTAWDMDFKGLCGEENPLIKLHKHMS 398

Qy 403 GDEKNSFECILGSPSTTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPT 458
Db 399 -----TYTVPARTGHTPTPEWARP-PTSPDPSGDPTPTPTPTPTPTPTPTPTPTPT 444

Qy 459 PTTTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPT 510
Db 445 TTTTARPTT-----TTTKVPHGTTEEDFDINVRPEVELPT-ENEVDNADV-CNSE 493

Qy 511 GP-IPHTNIHKYLVCFFVNGVNGWVHIMPCTPGTIW 545
Db 494 DDVVPDKKCSKYWC--VNGEGVQ--PSCQPGTIF 525

RESULT 9
O15993 PRELIMINARY; PRT; 467 AA.
ID O15993;
AC O15993;
DT 01-JAN-1998 (TremBLrel. 05, Created)
DT 01-JAN-1998 (TremBLrel. 05, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Fjchi-3.
OS Penaeus japonicus (Kuruma prawn).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
OC Penaeidae; Marsupenaeus.
OX NCBI_TaxID=27405;
RN [1]
RP SEQUENCE FROM N.A.
RA Watanabe T., Kono M., Aida K., Nagasawa H.;
RT "Purification and molecular cloning of a chitinase expressed in the
RL hepatopancreas of the penaeid prawn Penaeus japonicus.";
RL Biochim. Biophys. Acta 0:0-0(1997).
DR EMBL; AB008027; BAA22854.1;
DR HSP; P07254; ICTN.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008061; F:chitin binding; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0006030; P:chitin metabolism; IEA.
DR InterPro; IPR002557; Chitin_bind_PeR.
DR InterPro; IPR001223; Glyco_hydro_18.
DR InterPro; IPR001579; Glyco_hydro_18AS.
DR Pfam; PF01607; CBM 14; 1.
DR Pfam; PF00704; Glyco_hydro_18; 1.
DR ProDom; PD000471; Glyco_hydro_18; 1.
DR SMART; SM00494; ChitBD2; 1.
DR SMART; SM00636; Glyco_18; 1.
DR PROSITE; PS01095; CHITINASE 18; 1.
SQ SEQUENCE 467 AA; 51765 MW; 499F7095774CA445 CRC64;

Query Match 27.0%; Score 837.5; DB 5; Length 467;
Best Local Similarity 34.8%; Pred. No. 1.7e-44;
Matches 183; Conservative 85; Mismatches 173; Indels 85; Gaps 14;

Qy 35 IVCYVGTWTSYHK-VDPYTIEDIDPEKCTHLMYGFAXIDYKTIQVDFPYQD--DNHNS 91
Db 1 MCVYFGSWAVYRGLGKGFVEDIDPKICTHIVGFGAGL-AADSSIRVLPWNELCNNG- 58

Qy 92 WEKRGYERFNLRKNPELTMTISLGGWYEGSEKYSDMAANTYRQQTQSVDLQELQYK 151
Db 59 --KCAVDRFTALQQANLTKALLAVGWNESGPKYSKMAADPALNRKFTTSIELLKKG 116

Qy 152 FDGLDDWEYPGSRGNPKIDKONYLALVRELKDAFEPHYGLTAAVSPGKIDRAYDI 211
Db 117 FDGLDDWEYPTORGSGSD-DYDNFALLMAELKQALQPEGMILLTAASAGAKTIDPAYNV 175

Qy 212 KELNKLFDMMNMTYDYHGGWENFYGHNAPLYKRP-DETDELHTYFNNTMYHYLNNGA 270
Db 176 PEISKSLDLINVMYSLHGAWDYTHQSGLYAHPDDEGDL--YLNVDPAISYIEKGA 233
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QY 271 TRDKLVNVPYFGRAMSIEDRSKLGDPAGKMSPPGFISSGEGVLSYIELCOLFOKEEW 330
Db 234 RFGQIALGIPYRGWTLASQETGYAPAHQPGAGDWTSPGMLGNYEICYNTQTQDW 293
QY 331 HIQDEYVYAPYGV---NDKIVGWYDGLASISCKLAFELKELGSGVMVMSLENDDFKQHC 387
Db 294 TVDDPAMHEPYAYVFPNNWICSYDHAASVVTYAEYAKSKGLAGTWVNSVEDDFRGLC 353
QY 388 GPKNPLANKVHNMINGDEKNSFECILGFSITPTPTPTPTPTPTPTPTPTPTPTPTPT 447
Db 354 H-----NRKYLHI-----KTMVEVFGGSITP----- 376
QY 448 TPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPT 507
Db 377 -----PPLPTTRDPSEPTTTTRAPP-----PG-----IHC 403
QY 508 YKEDIHPTNIHKLVCPEF-VNCGWVHIMPCCPTGIMWCEKLTIC 552
Db 404 TTLGNLPPDLCTHYLCSLNTSGFDEKVEVCEGTLPNQPSPYC 449

RESULT 10
Q9GR93
ID Q9GR93 PRELIMINARY; PRT; 543 AA.
AC Q9GR93;
DT 01-MAR-2001 (TREMELrel. 16, Created)
DT 01-MAR-2001 (TREMELrel. 16, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Chitinase precursor (EC 3.2.1.14).
GN CHIB.
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
OC Bombycidae; Bombyx.
OX NCBI_TaxID=7091;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Kinshu x Showa; TISSUE=Integument;
RA Abdel-Banat B.M.A., Koga D.;
RT "Molecular cloning of Bombyx mori chitinase cDNA: a unique insert of 9
RT base pairs reduced the apparent molecular mass of the encoded
RT protein."
RL Submitted (DSC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB052914; BAB20017.1;
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008061; F:chitin binding; IEA.
DR GO; GO:0008843; F:endochitinase activity; IEA.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0006030; P:chitin metabolism; IEA.
DR InterPro; IPR002557; Chitin bind PerA.
DR InterPro; IPR001223; Glyco_hydro_18.
DR Pfam; PF01607; CBM_14; 1.
DR Pfam; PF00704; Glyco_hydro_18; 1.
DR ProDom; PD000471; Glyco_hydro_18; 1.
DR SMART; SM00494; ChtBD2; 1.
DR SMART; SM00636; Glyco_18; 1.
DR PROSITE; PS01095; CHITINASE_18; 1.
KW Glycosidase; Hydrolase; Signal.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 543 CHITINASE.
SQ SEQUENCE 543 AA; 60371 MW; C36C71E3B84DF88 CRC64;

Query Match
Best Local Similarity 27.0%; Score 837.5; DB 5; Length 543;
Matches 207; Conservative 78; Mismatches 208; Indels 83; Gaps 20;

QY 1 MKTIYAILSIMA-CIGLMNASIKRHDNDYKNPMRIVCYGTWGSVYHK-VDPYTIEDIP 58
Db 1 NRAIFATLAVLASCAALVQ-----SDSRARIVCYSNWAVYRPGVGRYGIEDIPV 50
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QY 59 FKCTHLMVGFAXIDEVKYTIQVDFPYQDDNHNHSEKRGYERFNNLRKLNPELTTWISLGG 118
Db 51 DLCTHLIVSFIQVTEKSEVLIIDPELD-----VDKSGFRNFTSRSRHPDVKFWAVGG 105
QY 119 WYEGSEKISDMAANFTYRQOFTSQSVLDLQEQYKFDGLDLDWEYPGSR-LGNFKIKQNYL 177
Db 106 WAEGGSKYSHWVAQKSTRMSFIRSVVDFLKKYDFDGLDLDWEYPGAADGGFSFKDKFL 165
QY 178 ALVRELKDAF--EPHGYLTAASVPGKOKIDRAYDIKLNKLFDWNNVMTYDHGWNF 235
Db 166 YFQELKRAFIRAGRWELTAAPLANFRLMGYHVPCLQELDALHVMVSYDLRGNWAGF 225
QY 236 YGHNAPLYKGPDETDELHTYFNVTMTYYLANGATRDKLVNVPYFGRAMSIED----- 290
Db 226 ADVHSFLYKRPD-QWAVEKLVNDELALWEEKGCTNKLKLVGIFPYGSRFSISAGNNY 284
QY 291 -----RSKLGDPAGKMSPPGFISSGEGVLSYIELCOLFOKE--EWHIQDEYVYAPY 342
Db 285 GLGTYNKEAGGDPAPYNTATP-----WAYEICEVDADGSGWTWKWDEFKQCY 337
QY 343 GYNDKIWGYDDLASISCKLAFELKELGSGVMVMSLENDDFKQHCQPKNPLANKVHNM 402
Db 338 AVKGTQWGYEDPRSVETKQWIKKGVILGANTWALDMDDFKGLCGEENPLKLLHRMS 397
QY 403 GDEKNSFECILGFSITPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPT 458
Db 398 -----THTVPPARTGHTTTPPEWARP-PSPTSDPSEGDPITPTTTTIVKPTT 443
QY 459 PTTTSPPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPT 510
Db 444 TRTARPTT-----TTTKVPHGTTEEDFINRPEVEELPT-ENEVDNADV-CNSE 492
QY 511 GP-IDPHTNIHKLVCPEFVNCGWVHIMPCCPTGIMWCEKLTIC 545
Db 493 DDYVPDKCEKSYKWC--VNCGVQ--FSCQPGTIF 524

RESULT 11
Q9GV05
ID Q9GV05 PRELIMINARY; PRT; 543 AA.
AC Q9GV05;
DT 01-MAR-2001 (TREMELrel. 16, Created)
DT 01-MAR-2001 (TREMELrel. 16, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Chitinase precursor (EC 3.2.1.14).
GN CHI.
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
OC Bombycidae; Bombyx.
OX NCBI_TaxID=7091;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Kinshu x Showa hybrid; TISSUE=Integument;
RX MEDLINE-21124800; PubMed-11222960;
RA Abdel-Banat B.M.A., Koga D.;
RT "A genomic clone for a chitinase gene from the silkworm, Bombyx mori:
RT structural organization identifies functional motifs.";
RL Insect Biochem. Mol. Biol. 31:497-508 (2001).
DR EMBL; AB048355; BAB13481.1;
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008061; F:chitin binding; IEA.
DR GO; GO:0008843; F:endochitinase activity; IEA.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0006030; P:chitin metabolism; IEA.
DR InterPro; IPR002557; Chitin bind PerA.
DR InterPro; IPR001223; Glyco_hydro_18.
DR Pfam; PF01607; CBM_14; 1.
DR Pfam; PF00704; Glyco_hydro_18; 1.
DR ProDom; PD000471; Glyco_hydro_18; 1.
DR SMART; SM00494; ChtBD2; 1.
DR SMART; SM00636; Glyco_18; 1.
KW Glycosidase; Hydrolase; Signal.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 543 CHITINASE.
SQ SEQUENCE 543 AA; 60371 MW; C36C71E3B84DF88 CRC64;
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[illegible]

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RESULT 12
P90710
ID P90710 PRELIMINARY; PRT; 565 AA.
AC P90710;
DT 01-MAY-1997 (T-EMBLrel. 03, Created)
DT 01-MAY-1997 (T-EMBLrel. 03, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Chitinase-like protein.
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Bombycoidea;
OC Bombycidae; Bombyx.
OX NCBI_TaxID=7091;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98318808; PubMed=9654739;
RA Kim M.G., Shin S.W., Bae K.S., Kim S.C., Park H.Y.;
RT "Molecular cloning of chitinase cDNAs from the silkworm, Bombyx mori
RT and the fall webworm, Hyphantria cunea.";
RL Insect Biochem. Mol. Biol. 28:163-171(1998).
DR EMBL: U86876; AAB47538.1; -

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GO; GO:0005576; C:extracellular; IEA.
 GO; GO:0008061; F:chitin binding; IEA.
 DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR GO; GO:0006030; P:chitin metabolism; IEA.
 DR InterPro; IPR002557; Chitin_bind_perA.
 DR InterPro; IPR001223; Glyco_Hydro_18.
 DR InterPro; IPR001579; Glyco_Hydro_18AS.
 DR Pfam; PF01607; CBM_14; 1.
 DR Pfam; PF00704; Glyco_hydro_18; 1.
 DR ProDom; PD000471; Glyco_hydro_18; 1.
 DR SMART; SM00494; ChtB2; 1.
 DR SMART; SM00636; Glyco_18; 1.
 DR PROSITE; PS01095; CHITINASE_18; 1.
 KW Glycosidase; Hydrolase.
 SQ SEQUENCE 565 AA; 63394 MW; 77D26D014875F3E2 CRC64;

Query Match 27.0%; Score 837.5; DB 5; Length 565;
 Best Local Similarity 35.9%; Pred.No.2.e-44;
 Matches 207; Conservative 78; Mismatches 208; Indels 83; Gaps 20;

QY 1 MKTIYAIIISMA-CIGLMMASIKRDNDYSKPMRIVCVGVTSVYHK-VDPYTIEDIDP 58
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 1 MRAIFATLAVLSAAALVQ-----SDSPARIVCYFSNWAVRPGVRGVIDIPV 50
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 59 FKCTHLMYGFAKDYEKKYIQVPDPYODDNHSWEKGYERFNLRKNPELTMTSLGG 118
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 51 DLCTHLIYFIGVTESSEVLIIDPELD----VDKSGRNFTSLSKHPDVCFMVAVGG 105
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 119 WTGESEKYSDMAANPYRRQQFOSVLDFQEYKFDEGLDWEPGSR-LGNPKLDKQNYL 177
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 106 WAEGGSYYSHWAQAQRSMFRSVDVFLKKYDFDGDLDDWVEPGAADRSGSFSDKDKFL 165
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 178 ALVRELKDAF--EPHGVLTAAYS PGKDKIDRAYDIKELNKLFDNMVMTYDYHGGWENF 235
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 166 YFVOELKRAFIRAGRWELTPAVPLANFRIMEGHYPVELCQELDAILHVMSYDLRGWAGF 225
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 236 YGHNAPLYKRPDDELHTVFNNYTMHYVLLNGNARDKLVMGVPFYGRAWSIED----- 290
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 226 ADVHSPLYKEPHD-QWAYEKLVNDGLNLWEEKGPCPNKLVGPIFYGRSFILLSAGNNY 284
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 291 -----RSKLKGDPKAGMSPPGFISEGEVLVYLCLQLPQKE--EWHIQDEYNAPY 342
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 285 GLGTYNKEAGGDPAPTYNTATGF-----WAYBEICTEVDADGGGWTKKWDEFCKCPY 337
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 343 GYNDKTVWGVDLASISKLAFLKELGVSVWMVSLENDDFKGCCEPKNLLANKVHNWIN 402
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 338 AYGKTOWGYEDPRSVEIKRNWKIEKGYLGAMTWAIDMDDFKGLCGEENFLIKLLHKHNS 397
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 403 GDEKNGFEICILGPSTTTPTTPTTPTTPTTPTTPTTPTT---TSPSTPTTPTTSPPT 458
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 398 -----NYTVPPARTGHTPTPWARP-PSTPSDSPGEDIPITTTTTVVKPPT 443
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 459 PTTPSPSTPTPTPTPTPTPTPTPTPTT-----HTSETPKYTYVDGHLIKCYKE 510
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 444 TRUTARPTT-----TTTKVPHGTEEDFDINVRAPEVELPT-ENEVDNAV-D-CNSE 492
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 511 GD-IPHEPTNHKYLVCFFNGCWVHWIMPCFGTIW 545
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 493 DDXYVPDKKCESKYWR--VNNEGVOQ--FSCQPSTIF 524
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

RESULT 13
 Q9VFR3 PRELIMINARY; PRT; 595 AA.

ID Q9VFR3 AC Q9VFR3
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBRel. 13, Last sequence update)
 DT 01-OCT-2003 (TrEMBRel. 25, Last annotation update)
 DE CG9307 protein (fp08984p).
 GN CG9307.
 OS Drosophila melanogaster (fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota:

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OC NCBI_TaxID=7227;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Anantides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blasej R.G., Champe V., Pfeiffer B.D.,
RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Mikos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Piankoc C., Baldwin D.,
RA Ballew R.M., Basu A., Bakendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlike C., Davenport L.B., Davies P.,
RA de Pablos C., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fessler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glaeser K.,
RA Glöckner A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Iqbal M.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Matrei B., McIntosh T.C., McLeod W.P., McPherson D.,
RA Morkulov G., Malshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Spier B.C., Sichen-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Snie E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissensbach J.,
RA Williams S.M., Woodgate T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhu G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhou S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of *Drosophila melanogaster*;"
RL Science 287:2185-2195(2000).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett P., Farfan D., Frise E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nunoo J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR ENBL; AEO03701; AAP54987.1; -;
DR EMBL; AV061553; AAL29101.1; -;
DR FlyBase; FBgn0038180; CG9307.
DR GO; GO:0005376; C:extracellular; IEA.
DR GO; GO:0008061; F:chitin binding; IEA.
DR GO; GO:0016798; F:hydrolyase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0005375; P:carbohydrate metabolism; IEA.
DR GO; GO:0006030; P:chitin metabolism; IEA.
DR InterPro; IPR002587; Chitin_bind_perA.
DR InterPro; IPR001223; Glyco_hydro_18.
DR InterPro; IPR001579; Glyco_hydro_18AS.
DR Pfam; PF01607; CBM_14; 1.
DR Pfam; PF00704; Glyco_hydro_18; 1.
DR ProDom; PD000471; Glyco_hydro_18; 1.
DR SMART; SM00434; ChitBD2; 1.
DR SMART; SM00636; Glyco_18; 1.
DR PROSITE; PS01095; CHITINASE_18; 1.
DR GO; GO:0005375; P:chitin metabolism; IEA.
DR GO:0005376; C:extracellular; IEA.
DR GO:0008061; F:chitin binding; IEA.
DR GO:0016798; F:hydrolyase activity, acting on glycosyl bonds; IEA.
DR GO:0005375; P:carbohydrate metabolism; IEA.
DR GO:0006030; P:chitin metabolism; IEA.
DR InterPro; IPR002587; Chitin_bind_perA.
DR InterPro; IPR001223; Glyco_hydro_18.
DR InterPro; IPR001579; Glyco_hydro_18AS.
DR Pfam; PF01607; CBM_14; 1.
DR Pfam; PF00704; Glyco_hydro_18; 1.
DR ProDom; PD000471; Glyco_hydro_18; 1.
DR SMART; SM00434; ChitBD2; 1.
DR SMART; SM00636; Glyco_18; 1.
DR PROSITE; PS01095; CHITINASE_18; 1.
DR GO; GO:0005375; P:chitin metabolism; IEA.
DR GO:0005376; C:extracellular; IEA.
DR GO:0008061; F:chitin binding; IEA.
DR GO:0016798; F:hydrolyase activity, acting on glycosyl bonds; IEA.
DR GO:0005375; P:carbohydrate metabolism; IEA.
DR GO:0006030; P:chitin metabolism; IEA.
DR InterPro; IPR002587; Chitin_bind_perA.
DR InterPro; IPR001223; Glyco_hydro_18.
DR InterPro; IPR001579; Glyco_hydro_18AS.
DR Pfam; PF01607; CBM_14; 1.
DR Pfam; PF00704; Glyco_hydro_18; 1.
DR ProDom; PD000471; Glyco_hydro_18; 1.
DR SMART; SM00434; ChitBD2; 1.
DR SMART; SM00636; Glyco_18; 1.
DR PROSITE; PS01095; CHITINASE_18; 1.
DR GO; GO:0005375; P:chitin metabolism; IEA.
DR GO:0005376; C:extracellular; IEA.
DR GO:0008061; F:chitin binding; IEA.
DR GO:0016798; F:hydrolyase activity, acting on glycosyl bonds; IEA.
DR GO:0005375; P:carbohydrate metabolism; IEA.
DR GO:0006030; P:chitin metabolism; IEA.
DR InterPro; IPR002587; Chitin_bind_perA.
DR InterPro; IPR001223; Glyco_hydro_18.
DR InterPro; IPR001579; Glyco_hydro_18AS.
DR Pfam; PF01607; CBM_14; 1.
DR Pfam; PF00704; Glyco_hydro_18; 1.
DR ProDom; PD000471; Glyco_hydro_18; 1.
DR SMART; SM00434; ChitBD2; 1.
DR SMART; SM00636; Glyco_18; 1.
DR PROSITE; PS01095; CHITINASE_18; 1.
DR GO; GO:0005375; P:chitin metabolism; IEA.
DR GO:0005376; C:extracellular; IEA.
DR GO:0008061; F:chitin binding; IEA.
DR GO:0016798; F:hydrolyase activity, acting on glycosyl bonds; IEA.
DR GO:0005375; P:carbohydrate metabolism; IEA.
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DR InterPro; IPR002587; Chitin_bind_perA.
DR InterPro; IPR001223; Glyco_hydro_18.
DR InterPro; IPR001579; Glyco_hydro_18AS.
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DR GO:0005376; C:extracellular; IEA.
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DR GO:0016798; F:hydrolyase activity, acting on glycosyl bonds; IEA.
DR GO:0005375; P:carbohydrate metabolism; IEA.
DR GO:0006030; P:chitin metabolism; IEA.
DR InterPro; IPR002587; Chitin_bind_perA.
DR InterPro; IPR001223; Glyco_hydro_18.
DR InterPro; IPR001579; Glyco_hydro_18AS.
DR Pfam; PF01607; CBM_14; 1.
DR Pfam; PF00704; Glyco_hydro_18; 1.
DR ProDom; PD000471; Glyco_hydro_18; 1.
DR SMART; SM00434; ChitBD2; 1.
DR SMART; SM00636; Glyco_18; 1.
DR PROSITE; PS01095; CHITINASE_18; 1.
DR GO; GO:0005375; P:chitin metabolism; IEA.
DR GO:0005376; C:extracellular; IEA.
DR GO:0008061; F:chitin binding; IEA.
DR GO:0016798; F:hydrolyase activity, acting on glycosyl bonds; IEA.
DR GO:0005375; P:carbohydrate metabolism; IEA.
DR GO:0006030; P:chitin metabolism; IEA.
DR InterPro; IPR002587; Chitin_bind_perA.
DR InterPro; IPR001223; Glyco_hydro_18.
DR InterPro; IPR001579; Glyco_hydro_18AS.
DR Pfam; PF01607; CBM_14; 1.
DR Pfam; PF00704; Glyco_hydro_18; 1.
DR ProDom; PD000471; Glyco_hydro_18; 1.
DR SMART; SM00434; ChitBD2; 1.
DR SMART; SM00636; Glyco_18; 1.
DR PROSITE; PS01095; CHITINASE_18; 1.
DR GO; GO:0005375; P:chitin metabolism; IEA.
DR GO:0005376; C:extracellular; IEA.
DR GO:0008061; F:chitin binding; IEA.
DR GO:0016798; F:hydrolyase activity, acting on glycosyl bonds; IEA.
DR GO:0005375; P:carbohydrate metabolism; IEA.
DR GO:0006030; P:chitin metabolism; IEA.
DR InterPro; IPR002587; Chitin_bind_perA.
DR InterPro; IPR001223; Glyco_hydro_18.
DR InterPro; IPR001579; Glyco_hydro_18AS.
DR Pfam; PF01607; CBM_14; 1.
DR Pfam; PF00704; Glyco_hydro_18; 1.
DR ProDom; PD000471; Glyco_hydro_18; 1.
DR SMART; SM00

Query Match	27.0%;	Score	837.5;	DB	5;	Length	595;
Best Local Similarity	35.2%;	Pred.	No. 2.3e-44;				
Matches	201;	Conservative	84;	Mismatches	199;	Indels	87;
Gaps	22;						
QY	29	SKNPMRIIVCVGWSVYHK	-VDPYTTEDDPFKCTHLMYGFADIKDYSKVYTIQVFDPPQDD	87			
DB	23	SDQASRIIVCFNSWAVYRTIGRYGLIEDVPADLCTHIIYSFIGVNDKSDWDLVIDELD	-81				
QY	88	NHNSWEKRGYERFNNLURLKNPELTTMISLGGWYEGSEKYSYDMAANPTYRQOFTQSVLDLFL	147				
DB	82	---VDQGGFSKFTQLKSNPNVKLEIAVGGMAEGGSKYSQWAVADRDRSQSFIRSVVRFM	137				
QY	148	QYKYPGLDLIDWEYPSG--RLGNPKDKQNYLALVRELKDAF--EPHGYYLLTAAVSVSGKD	203				
DB	138	KQYNFDFGLDWEYPGATDRGGNYG-DKQFLYFVBEELRAAFDRGRGWEITWAVPVAKF	196				
QY	204	KIDRAYDIKELNKLFDWMNVMTVDYHGGWENFYGHNAPLYKRPDDELTHTYNNVNTMH	263				
DB	197	RLNEGHYHVELCEALDAIHANTYDLRGNWAGFADVHSPLYKRKH-D-QAYEKLNVNDGLA	255				
QY	264	YYLNGGATDKLVMGVYFYGRAWISIDRSK-LKLK---DPAKGMSPPGFISGEEGLSYI	319				
DB	256	LWEEMGPCANKLVGVYFYGRTFTLSNKNVNGTYINKEAGGAPGPGYTNASGLLAY	315				
QY	320	ELC-QLFQKEB-WHIQVDEYNNAPYNDKIWGYDDLASISCKLAPFLKELGVSGVWWS	377				
DB	316	EICTEYMDKSKGTVWEWDAGMVPYTYKDTQWYGVENEASIQIKMDPIKORGYAGAMTWA	375				
QY	378	LENDDEPKHGCGPNPLLNKVH-NWINGDEKNSFECILGPSTPTTPTTTP--TTPTTT	432				
DB	376	IDMDDPHGCGRKNGLTQILYDNMKN-----YRVPEPTROTTPRPEWAKPPAT	423				
QY	433	PTTP-----SPTPTT-----TPSPPTTPTTTPS--PTTPTTTPSPTTPTTPTTP--	473				
DB	424	PNPDEGAVVAPTSTTKRPKPKPTSSPLSPTSAPGPVTVGSSPTPKPTTKPKPKPK	483				
QY	474	TPAPTTSPSTPTTEHTSEPKYTTY-----VDGHLIKCYKEGDIPHP	516				
DB	484	TTTTTTTTTAP---EKSTBEPSEWYVPDVEPTDPEQPMQPGDPDNEICTNRDVFVHP	540				
QY	517	TNIHKVLVCFVNGVWVHIMP-----CPPGT	543				
DB	541	-NCRKYFR-----VHGKPYFECKEGT	562				
RESULT	14						
Q9W2M7		PRELIMINARY;	PRT;	450	AA.		
AC	Q9W2M7						
DT	01-MAY-2000	(T-EMBLrel. 13, Created)					
DT	01-MAY-2000	(T-EMBLrel. 13, Last sequence update)					
DT	01-OCT-2003	(T-EMBLrel. 25, Last annotation update)					
DE	CG9357	protein.					
CS	CG9357						
OS	Drosophila melanogaster	(Fruit fly).					
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;						
OC	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;						
OC	Ephydroidea; Drosophilidae; Drosophila.						
OX	NCBI_TaxID=7227;						
RN	[1]						
RP	SEQUENCE FROM N.A.						
RC	STRAIN=Berkeley.						
RX	MEDLINE=20196006; PubMed=10731132;						
RA	Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,						
RA	Ananatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,						
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,						
RA	Sutton G.G., Wortman J.R., Zhang M.D., Zhang Q., Chen L.X.,						
RA	Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,						
RA	Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,						
RA	Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,						
RA	Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,						
RA	Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,						

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahle C., Davenport L.B., Davies P.,
RA De Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrera S., Fleischmann W.,
RA Foslæk A., Gabriëlian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mactel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svitskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL; AF003452; AAF46663.1; -.
DR FSSP; P07254; 1C7N.
DR FlyBase; FBgn0034580; CG9357.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008061; F:chitin binding; IEA.
DR GO; GO:0015798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0006030; P:chitin metabolism; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR InterPro; IPR002557; Chitin bind PerA.
DR InterPro; IPR001179; FKBP_PPIase.
DR InterPro; IPR001223; Glyco_hydro_18.
DR InterPro; IPR001579; Glyco_hydro_18AS.
DR Pfam; PF01607; CBM_14; 1.
DR Pfam; PF00704; Glyco_hydro_18; 1.
DR ProDom; PD000471; Glyco_hydro_18; 1.
DR SMART; SM00494; ChtBD2; 1.
DR SMART; SM00636; Glyco_18; 1.
DR PROSITE; PS01095; CHITINASE_18; 1.
DR PROSITE; PS00453; FKBP_PPIASE_1; 1.
KW Glycosidase; Hydrolase.
SQ SEQUENCE 460 AA; 51055 MW; 8EF4F126F1DD8D9B CRC64;

Query Match 26.8%; Score 832; DB 5; Length 460;
Best Local Similarity 33.7%; Pred. No. 3.7e-44;
Matches 183; Conservative 87; Mismatches 175; Indels 98; Gaps 11;

QY 17 MNASIKRDNDSKPMRVCVGVGWSVYHK-VDPYTTIEDIDPFKCHLMYGFPAKIDRYK 75
DB 1 MAASSAQGNS-SKN---VVCVQGTWSVYRPGKFGMEDIDPFKCHLMYGFPAKIDRYK 55

QY 76 YTIQVDPYDDNHNSEWKGVERFNRLKPKELTMTISLGWYEGSEKYSMDAANPTY 135
DB 56 GQURVDAVDLLENS-GRGNTKSNFALKPKNPVUKTVAVGGWNEGKRSLVARDPSK 114

QY 136 RQOFIQSLVDLQYKFGDGLDWEYPPGSRGKGNPKIDKQNYLALVRELKDAPEPHGYLLT 195
DB 115 REKFVDDVYRQRHGFDGLDWEYPPGSRGKGNPKIDKQNYLALVRELKDAPEPHGYLLT 174

QY 196 AAVSPGKIDIRAYDIKELNKLFDWNNVTYHGWENFYGHNPAYL---KRPDETDEL 252
DB 175 AAVGSAQFSAEISYDIPAMVPVLDLINVMAVDLHGPWDQVGINAPLYAAEKDASDSSGR 234

QY 253 HYFENVYNTWYLLNNGATEDKLVMGVPYFGWANSIEDRSKLKLGDPKAGMSPPFGISGE 312

DB 235 QOQLNVDAVVKYLKAGAPAEKILGVFPYGRSFTLATAGNQPGAPHIGKGIAGNYSRE 294
QY 313 EGVLSVIELCQIFQKEWEHIQDEYNAPYGNKDIWYDGLASISCKLAFELKELGVSG 372
DB 295 PGVLGNELCEMERBEWTKWEATQQVEYAYRQWGVYEDERSLAKAQYVMDNLGG 354
QY 373 VMVNSLENDDFKHGCGPK-NPILNKVHNNGDEKNSFECILGSPSTTTTPTTPTPTT 431
DB 355 IMIWSLESDDFRGTCQGGQPYPLLHEINRVLFGG-----NTPSLGTTESNR 387
QY 432 TPTTSPPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTT 491
DB 388 -----NTPSLGTTESNR 399

QY 492 ETPK--YTTVGDHLIKYKGBDIPHTNIHKYLVCFVNGWVHIMPCTGTCWCQSK 549
DB 400 ESESEGFSCPADA-----PAGVIRPDNCKSFYVC-----SGKTHNFCPSGLNFDLDT 449
QY 550 LTC 552
DB 450 KSC 452

RESULT 15
Q8ITU3 PRELIMINARY; PRT; 467 AA.
AC Q8ITU3;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Chitinase.
OS Penaeus vannamei (Penaeid shrimp) (European white shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
OC Penaeidae; Litopenaeus.
OC NCBI_TaxID=6689;
RN [1]
RP SEQUENCE FROM N.A.
RA Chang R.C.;
RT Cloning and characterization of a cDNA encoding a chitinase from
RT hepatopancreas of the Penaeus vannamei (Crustacea, Decapoda).";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF315689; AAN74647.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008061; F:chitin binding; IEA.
DR GO; GO:0015787; F:hydrolase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0006030; P:chitin metabolism; IEA.
DR InterPro; IPR002557; Chitin bind PerA.
DR InterPro; IPR001223; Glyco_hydro_18.
DR InterPro; IPR001579; Glyco_hydro_18AS.
DR Pfam; PF01607; CBM_14; 1.
DR Pfam; PF00704; Glyco_hydro_18; 1.
DR ProDom; PD000471; Glyco_hydro_18; 1.
DR SMART; SM00494; ChtBD2; 1.
DR SMART; SM00636; Glyco_18; 1.
DR PROSITE; PS01095; CHITINASE_18; 1.
DR PROSITE; PS00453; FKBP_PPIASE_1; 1.
SQ SEQUENCE 467 AA; 51958 MW; 734A830C6FA7F4CD CRC64;

Query Match 26.8%; Score 831.5; DB 5; Length 467;
Best Local Similarity 34.2%; Pred. No. 4.1e-44;
Matches 180; Conservative 87; Mismatches 174; Indels 85; Gaps 14;

QY 35 IVCVGVGWSVYHK-VDPYTTIEDIDPFKCHLMYGFPAKIDRYKTIQVFPYQD--DNHNS 91
DB 1 MCVCFGSAAYRQGLGKFDVEDIDPKICTHIIFGFAGL-AHDSIRVLDPNWLCDNYG- 58

QY 92 WEKRGIFERNLRLKPKELTMTISLGWYEGSEKYSMDAANPTYRQOFLOSVDLFLQYK 151
DB 59 --KCAVDRFTALKQONANKAILAVGGWNEGSPKSKMAADPVLNRNRTSSIELKKKG 116

QY 152 FDGLDLDWEYPPGSRGKGNPKIDKQNYLALVRELKDAPEPHGYLLTAAVSPGKDKIDRYDI 211

Search completed: March 22, 2004, 06:59:24
Job time : 113.679 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 22, 2004, 06:30:23 ; Search time 168.752 Seconds
(without alignments)
929.256 Million cell updates/sec

Title: US-09-662-293-15

Perfect score: 3107
Sequence: 1 MKTIYAILSIMAGIGLWNAS.....IMPCPPGTWCQKLTICGE 555

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Van04:*
1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001s:*
5: Geneseq2002s:*
6: Geneseq2003as:*
7: Geneseq2003bs:*
8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3107	100.0	555	3 AAY52523	House dust mite
2	3107	100.0	555	5 AAU96327	Der HMW-m
3	3107	100.0	555	5 AAU96328	Der HMW-m
4	3014	97.0	536	3 AAY52525	House dust
5	3014	97.0	536	5 AAU96329	Der HMW-m
6	2542	81.8	509	3 AAY52533	D. pteron
7	2542	81.8	509	5 AAU96337	Der HMW-m
8	2542	81.8	509	5 AAU96338	Der HMW-m
9	2475	79.7	490	3 AAY52535	D. pteron
10	2475	79.7	490	5 AAU96339	Der HMW-m
11	1008.5	32.5	525	6 ABP72636	Anopheles
12	854.5	27.5	498	4 ABB58595	Drosophila
13	838.5	27.0	554	2 AAU01824	Manduca s
14	838.5	27.0	554	3 AAB07183	Manduca s
15	838.5	27.0	554	6 ABP72619	Manduca s
16	837.5	27.0	467	6 ABP72634	Prawn chi
17	837.5	27.0	555	6 ABP72625	Bombus no
18	837.5	27.0	595	4 ABB71737	Drosophila
19	832	26.8	460	4 ABB54366	Drosophila
20	815.5	26.2	583	5 AAE28197	Flea chit
21	812.5	26.2	635	5 AAE28203	Flea chit
22	811.5	26.1	559	5 AAE28199	Flea PCFC
23	810	26.1	574	6 ABP72635	Aedes aeg
24	802	25.8	483	6 ABP72633	Chelonus
25	787	25.3	553	6 ABP72626	Hyphantri

26	738	23.8	466	2 AAW08584	Human 50
27	738	23.8	466	2 AAW40259	Human chi
28	738	23.8	466	2 AAY42425	MO-218 cl
29	738	23.8	466	4 AAE00432	Human chi
30	738	23.8	466	5 AAE25903	Human chi
31	738	23.8	466	5 ABB76291	Human chi
32	737.5	23.7	520	6 ABU09914	Partial m
33	736.5	23.7	473	7 ABR55543	Amino aci
34	735.5	23.7	459	7 ADC24231	Human NOV
35	734.5	23.6	473	7 ADC51464	Chitotria
36	732.5	23.6	387	2 AAW08585	Human 39
37	732	23.6	447	7 ADC24237	Human NOV
38	732	23.6	466	2 AAW40260	Human chi
39	732	23.6	466	2 AAY42426	MO-13B cl
40	732	23.6	466	4 AAE00433	Human chi
41	732	23.6	466	5 AAE25904	Human chi
42	732	23.6	466	5 ABB76292	Human chi
43	731	23.5	466	2 AAW31498	Human chi
44	729.5	23.5	452	7 ABR55544	Amino aci
45	723	23.3	466	6 ABP72621	Human chi

ALIGNMENTS

RESULT 1

AY52523	standard; protein, 555 AA.
ID	AY52523 standard; protein, 555 AA.
XX	XX
AC	AY52523;
XX	XX
DT	22-FEB-2000 (first entry)
DE	House dust mite (D. farinae) mite allergen protein (map) PDerf98-555.
XX	XX
KW	Mite allergen protein; map; high molecular weight; HMW-map; allergy;
KW	house dust mite; IGE, immunoglobulin E; allergen; mapA; mapB;
KW	hypersensitivity reaction; therapy; diagnosis; human; feline;
KW	canine; veterinary; antibody; vaccine; immunisation.
XX	XX
OS	Dermatophagoides farinae.
XX	XX
PH	Key Location/Qualifiers
FT	Peptide 1..19
FT	/note= "Signal peptide"
FT	Protein 20..555
FT	/note= "Mature PDerf98-555"
XX	XX
FN	WO9954349-A2.
XX	XX
PD	28-OCT-1999.
XX	XX
PF	16-APR-1999; 99WO-US008524.
XX	XX
PR	17-APR-1998; 98US-00062013.
PR	13-MAY-1998; 98US-0085295P.
PR	02-SEP-1998; 98US-0098909P.
XX	XX
PA	(HESK-) HESKA CORP.
XX	XX
PI	Mccall CA, Hunter SW, Weber ER;
XX	XX
DR	WPI; 2000-052700/04.
DR	N-PSDB; AAZ38575, AAZ38576, AAZ38577, AAZ38578.
XX	XX
FT	Novel high molecular weight Dermatophagoides nucleic acid polypeptides
FT	used to modify an animals' hypersensitivity to mite allergens.
XX	XX
PS	Claim 3; Page 111-113; 154pp; English.
XX	XX
CC	This sequence represents Dermatophagoides farinae mite allergen protein
CC	(map) PDerf98-555. PDerf98-555 has a molecular weight of 98 kD,
CC	comprising 555 amino acids, and is a component of the Dermatophagoides

CC farinae high molecular weight mite allergen protein (HWM-map)
 CC composition. The HWM-map composition was isolated from a D. farinae
 CC homogenate by gel filtration, with each fraction being analysed for the
 CC presence of proteins that bound to IgE present in mite-allergic dog
 CC antisera. Mite allergenic proteins and peptides, and nucleic acids
 CC encoding them, may be used in therapeutic compositions to modify an
 CC animal's hypersensitivity reaction to mite allergens. Animals that may be
 CC treated include mammals and birds, especially felines, canines, equines,
 CC humans, other pets, and work or domestic animals. The proteins or
 CC fragments may also be used to diagnose allergies via a skin test. The
 CC proteins and peptides can also be used to raise antibodies, which have a
 CC variety of potential uses. For example, they can be used as vaccines to
 CC passively immunise animals against dust mite hypersensitivity, as
 CC positive controls in test kits and as tools to recover desired dust mite
 CC allergens from a mixture of proteins
 XX
 XX Sequence 555 AA;

Query Match 100.0%; Score 3107; DB 3; Length 555;
 Best Local Similarity 100.0%; Pred. No. 1.8e-217;
 Matches 555; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKTIYAILSIMACIGLMNASIKRDNDYSKNPMRIVCVGTWSVYHKVDPTTIEDIDPFK 60
 Db 1 MKTIYAILSIMACIGLMNASIKRDNDYSKNPMRIVCVGTWSVYHKVDPTTIEDIDPFK 60
 QY 61 CTHLMYGFPAKIDYKTIQVDFPDQDDNHSWEKRGYERFNNLRKLNPELTMTISLGWY 120
 Db 61 CTHLMYGFPAKIDYKTIQVDFPDQDDNHSWEKRGYERFNNLRKLNPELTMTISLGWY 120
 QY 121 EGSKYSDMAANPYRQOFTQSULDFLOEYKFDGLDWEYPSGRINPKIDKQNYALV 180
 Db 121 EGSKYSDMAANPYRQOFTQSULDFLOEYKFDGLDWEYPSGRINPKIDKQNYALV 180
 QY 181 RELKDAPEPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYGWENFYGHNA 240
 Db 181 RELKDAPEPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYGWENFYGHNA 240
 QY 241 PLYKRPDETDLHTYFNNVTMHHYLLNNGATRDKLVMGVFFYGRAWSIEDRSKLGDDPA 300
 Db 241 PLYKRPDETDLHTYFNNVTMHHYLLNNGATRDKLVMGVFFYGRAWSIEDRSKLGDDPA 300
 QY 301 KGMSPPGFISGEEGVLSEIQLCFQKEWHIQYDEYNNAPYGYNDKIWGYDDLASISC 360
 Db 301 KGMSPPGFISGEEGVLSEIQLCFQKEWHIQYDEYNNAPYGYNDKIWGYDDLASISC 360
 QY 361 KLAFLKELGVSGVMWSLENDDFKGGCPKNDKIDRAYDIKELNKLFDWMNVMTYDYGWENFYGHNA 420
 Db 361 KLAFLKELGVSGVMWSLENDDFKGGCPKNDKIDRAYDIKELNKLFDWMNVMTYDYGWENFYGHNA 420
 QY 421 TPPTTPT 480
 Db 421 TPPTTPT 480
 QY 481 TSPPTTTEHTSETPKYTYVDGHLIKVCYKEGDIHPNTNHHKLVCFEFGWGWVHIMPCP 540
 Db 481 TSPPTTTEHTSETPKYTYVDGHLIKVCYKEGDIHPNTNHHKLVCFEFGWGWVHIMPCP 540
 QY 541 PGTIWCQEKLCIG 555
 Db 541 PGTIWCQEKLCIG 555

RESULT 2
 AAU96327
 ID AAU96327 standard; protein; 555 AA.

XX AC AAU96327;
 XX 15-JUL-2002 (first entry)
 DT Der HWM-map polypeptide #14.

KW Der HWM-map; American house dust mite; antiallergic; mite; IgE;
 KW mite allergenic protein; immunoglobulin E; hypersensitivity;
 KW immunocomplex formation.
 OS Dermatophagoides farinae.
 XX WO200222807-A2.
 XX 21-MAR-2002.
 PD 14-SEP-2001; 2001WO-US028730.
 PF 14-SEP-2000; 2000US-00662293.
 PR (HESK-) HESKA CORP.
 XX
 XX Mccall CA, Hunter SW, Weber ER;
 XX WPI; 2002-351888/38.
 DR N-PSDB; ABK69571.
 XX
 PT New mite allergenic protein isolated from Dermatophagoides, designated
 PT Der HWM-map protein, useful as a vaccine for treating mite allergy.
 PS Claim 12; Page 114-116; 16:pp; English.
 XX
 CC The invention relates to an isolated mite allergenic protein of
 CC Dermatophagoides, designated Der HWM-map protein, and its related nucleic
 CC acid. The Der HWM-map protein is useful for eliciting an immune response
 CC against Der HWM-map protein. The protein or a reagent comprising a non-
 CC proteinaceous epitope is useful for identifying an animal (e.g., dog,
 CC cat) susceptible to or having an allergic response to a mite. A
 CC therapeutic composition is useful for desensitising a host animal to an
 CC allergic response to a mite. The DNA and protein can be used in the
 CC detection of anti-Der HWM-map antibodies in animal fluids, and inhibition
 CC of immunoglobulin (Ig)E or Der HWM-map protein activity associated with a
 CC disease. Antibodies that bind to Der HWM-map are useful for inhibiting
 CC binding of proteins to IgE, to prevent immunocomplex formation, thus
 CC reducing hypersensitivity responses to mite allergens, and as vaccines
 CC against mite allergen hypersensitivity. Sequences AAU96314-AAU96342
 CC represent Der HWM-map polypeptides of the invention
 XX
 SQ Sequence 555 AA;
 Query Match 100.0%; Score 3107; DB 5; Length 555;
 Best Local Similarity 100.0%; Pred. No. 1.8e-217;
 Matches 555; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKTIYAILSIMACIGLMNASIKRDNDYSKNPMRIVCVGTWSVYHKVDPTTIEDIDPFK 60
 Db 1 MKTIYAILSIMACIGLMNASIKRDNDYSKNPMRIVCVGTWSVYHKVDPTTIEDIDPFK 60
 QY 61 CTHLMYGFPAKIDYKTIQVDFPDQDDNHSWEKRGYERFNNLRKLNPELTMTISLGWY 120
 Db 61 CTHLMYGFPAKIDYKTIQVDFPDQDDNHSWEKRGYERFNNLRKLNPELTMTISLGWY 120
 QY 121 EGSKYSDMAANPYRQOFTQSULDFLOEYKFDGLDWEYPSGRINPKIDKQNYALV 180
 Db 121 EGSKYSDMAANPYRQOFTQSULDFLOEYKFDGLDWEYPSGRINPKIDKQNYALV 180
 QY 181 RELKDAPEPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYGWENFYGHNA 240
 Db 181 RELKDAPEPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYGWENFYGHNA 240
 QY 241 PLYKRPDETDLHTYFNNVTMHHYLLNNGATRDKLVMGVFFYGRAWSIEDRSKLGDDPA 300
 Db 241 PLYKRPDETDLHTYFNNVTMHHYLLNNGATRDKLVMGVFFYGRAWSIEDRSKLGDDPA 300
 QY 301 KGMSPPGFISGEEGVLSEIQLCFQKEWHIQYDEYNNAPYGYNDKIWGYDDLASISC 360
 Db 301 KGMSPPGFISGEEGVLSEIQLCFQKEWHIQYDEYNNAPYGYNDKIWGYDDLASISC 360
 QY 361 KLAFLKELGVSGVMWSLENDDFKGGCPKNDKIDRAYDIKELNKLFDWMNVMTYDYGWENFYGHNA 420
 Db 361 KLAFLKELGVSGVMWSLENDDFKGGCPKNDKIDRAYDIKELNKLFDWMNVMTYDYGWENFYGHNA 420

DR WPI; 2000-052700/04.
DR N-PSDB; AAZ38579, AAZ38580.
XX Novel high molecular weight Dermatophagoides nucleic acid polypeptides
PT used to modify an animals' hypersensitivity to mite allergens.
XX
XX Claim 3; Page 125-127; 154pp; English.
XX
XX This sequence represents Dermatophagoides farinae mite allergen protein
CC (map) pDerf98-536, the mature form of pDerf98-555 (AAV52523). pDerf98-536
CC has a molecular weight of 98 kD, comprising 536 amino acids, and is a
CC component of the Dermatophagoides farinae high molecular weight mite
CC allergen protein (HWM-map) composition. The HWM-map composition was
CC isolated from a D. farinae homogenate by gel filtration, with each
CC fraction being analysed for the presence of proteins that bound to IgE
CC present in mite-allergic dog antisera. Mite allergenic proteins and
CC peptides, and nucleic acids encoding them, may be used in therapeutic
CC compositions to modify an animal's hypersensitivity reaction to mite
CC allergens. Animals that may be treated include mammals and birds,
CC especially felines, canines, equines, humans, other pets, and work or
CC domestic animals. The proteins or fragments may also be used to diagnose
CC allergies via a skin test. The proteins and peptides can also be used to
CC raise antibodies, which have a variety of potential uses. For example,
CC they can be used as vaccines to passively immunise animals against dust
CC mite hypersensitivity, as positive controls in test kits and as tools to
CC recover desired dust mite allergens from a mixture of proteins
XX
XX Sequence 536 AA;
XX
Query Match 97.0%; Score 3014; DB 3; Length 536;
Best Local Similarity 100.0%; Pred. No. 1e-210;
Matches 536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 20 SIKRDHNDYKSNPRIVCYVGTWVYHKVDPTTIEDIDPFKCTHLMYGFPAKIDYKTYIQ 79
Db 1 SIKRDHNDYKSNPRIVCYVGTWVYHKVDPTTIEDIDPFKCTHLMYGFPAKIDYKTYIQ 60
QY 80 VFDPYQDDNHNWSEKRGYERFNNLRKKNPELTMTISLGWYEGSEKYSMDAANPTYRQOF 139
Db 61 VFDPYQDDNHNWSEKRGYERFNNLRKKNPELTMTISLGWYEGSEKYSMDAANPTYRQOF 120
QY 140 IQSVLDFLOEYKFDGLDLDWEYPSGRLGNPKIDKQNYALVRELKDAFEPHGVLTTAAVS 199
Db 121 IQSVLDFLOEYKFDGLDLDWEYPSGRLGNPKIDKQNYALVRELKDAFEPHGVLTTAAVS 180
QY 200 PGKDKIDRAYDIKELNKLFDWMVNTYDYGWENFYGHNAPLYKRPDETDELHTYFNVN 259
Db 181 PGKDKIDRAYDIKELNKLFDWMVNTYDYGWENFYGHNAPLYKRPDETDELHTYFNVN 240
QY 260 YTHMYLLNNGATRDKLVGVDPFYGRAWSIEDRSKLGDPAGKMSPPGFISSGEGVLSYI 319
Db 241 YTHMYLLNNGATRDKLVGVDPFYGRAWSIEDRSKLGDPAGKMSPPGFISSGEGVLSYI 300
QY 320 ELCQLFQKEEWHIOYDEVYNAPYGNDKIWGYDDLASISCKLAFLKELGVSGVWMSLE 379
Db 301 ELCQLFQKEEWHIOYDEVYNAPYGNDKIWGYDDLASISCKLAFLKELGVSGVWMSLE 360
QY 380 NDDFKHGCGPKNPLLNKVNHNMDKNSFECILGPSTTPTPTTPTTPTTPTTPTTPTTPT 439
Db 361 NDDFKHGCGPKNPLLNKVNHNMDKNSFECILGPSTTPTPTTPTTPTTPTTPTTPTTPT 420
QY 440 TPTTPT 499
Db 421 TPTTPT 480
QY 500 VDGHILKCYKEGDIHPHTNIHKYLCVFVNGWVWHIMPCPGFIHWCQEKLTICGE 555
Db 481 VDGHILKCYKEGDIHPHTNIHKYLCVFVNGWVWHIMPCPGFIHWCQEKLTICGE 536
RESULT 5
AAU96329
ID AAU96329 standard; protein; 536 AA.

XX AAU96329;
XX AC
XX DT 15-JUL-2002 (first entry)
XX DE
XX Der HWM-map polypeptide #16.
XX
XX Der HWM-map; American house dust mite; antiallergic; mite; IgE;
KW mite allergenic protein; immunoglobulin E; hypersensitivity;
KW immunocomplex formation.
XX
XX Dermatophagoides farinae.
OS
XX WO200222807-A2.
PN
XX 21-MAR-2002.
PD
XX
XX 14-SEP-2001; 2001WO-US028730.
PF
XX
XX 14-SEP-2000; 2000US-00662293.
PR
XX
XX (HESK-) HESKA CORP.
PA
XX McCall CA, Hunter SW, Weber ER;
PI
XX
XX WPI: 2002-351888/38.
DR
XX N-PSDB; ABK69575.
DR
XX
XX New mite allergenic protein isolated from Dermatophagoides, designated
PT Der HWM-map protein, useful as a vaccine for treating mite allergy.
PT
XX
XX Claim 12; Page 125-127; 161pp; English.
PS
XX
XX The invention relates to an isolated mite allergenic protein of
CC Dermatophagoides, designated Der HWM-map protein, and its related nucleic
CC acid. The Der HWM-map protein is useful for eliciting an immune response
CC against Der HWM-map protein. The protein or a reagent comprising a non-
CC proteinaceous epitope is useful for identifying an animal (e.g., dog,
CC cat) susceptible to or having an allergic response to a mite. A
CC therapeutic composition is useful for desensitising a host animal to an
CC allergic response to a mite. The DNA and protein can be used in the
CC detection of anti-Der HWM-map antibodies in animal fluids, and inhibition
CC of immunoglobulin (Ig)E or Der HWM-map protein activity associated with a
CC disease. Antibodies that bind to Der HWM-map are useful for inhibiting
CC binding of proteins to IgE, to prevent immunocomplex formation, thus
CC reducing hypersensitivity responses to mite allergens, and as vaccines
CC against mite allergen hypersensitivity. Sequences AAU96314-AAU96342
CC represent Der HWM-map polypeptides of the invention
XX
XX Sequence 536 AA;
XX
Query Match 97.0%; Score 3014; DB 5; Length 536;
Best Local Similarity 100.0%; Pred. No. 1e-210;
Matches 536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 20 SIKRDHNDYKSNPRIVCYVGTWVYHKVDPTTIEDIDPFKCTHLMYGFPAKIDYKTYIQ 79
Db 1 SIKRDHNDYKSNPRIVCYVGTWVYHKVDPTTIEDIDPFKCTHLMYGFPAKIDYKTYIQ 60
QY 80 VFDPYQDDNHNWSEKRGYERFNNLRKKNPELTMTISLGWYEGSEKYSMDAANPTYRQOF 139
Db 61 VFDPYQDDNHNWSEKRGYERFNNLRKKNPELTMTISLGWYEGSEKYSMDAANPTYRQOF 120
QY 140 IQSVLDFLOEYKFDGLDLDWEYPSGRLGNPKIDKQNYALVRELKDAFEPHGVLTTAAVS 199
Db 121 IQSVLDFLOEYKFDGLDLDWEYPSGRLGNPKIDKQNYALVRELKDAFEPHGVLTTAAVS 180
QY 200 PGKDKIDRAYDIKELNKLFDWMVNTYDYGWENFYGHNAPLYKRPDETDELHTYFNVN 259
Db 181 PGKDKIDRAYDIKELNKLFDWMVNTYDYGWENFYGHNAPLYKRPDETDELHTYFNVN 240
QY 260 YTHMYLLNNGATRDKLVGVDPFYGRAWSIEDRSKLGDPAGKMSPPGFISSGEGVLSYI 319
Db 241 YTHMYLLNNGATRDKLVGVDPFYGRAWSIEDRSKLGDPAGKMSPPGFISSGEGVLSYI 300

Db 241 YTMHYIANNAGTRDKLVGMVPPFYGRAWSIEDRSKXKLGDPKAGMSPPGFTSGEGVLSYI 300
Qy 320 ELQQLFQKEBWHIQDEYNNAPYGYNDKIWGVYDDIASISCKLAFKELGVSQVWWSLE 379
Db 301 ELQQLFQKEBWHIQDEYNNAPYGYNDKIWGVYDDIASISCKLAFKELGVSQVWWSLE 360
Qy 380 NDDFKHCGKPNLLKVNHWINGDEKNSPECILGSPSTTPTTPTTPTTPTTPTTPTT 439
Db 361 NDDFKHCGKPNLLKVNHWINGDEKNSPECILGSPSTTPTTPTTPTTPTTPTTPTT 420
Qy 440 TPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTT 499
Db 421 TPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTT 480
Qy 500 VDGHILKYKEGDIPIHPTNIHKYLVCFFVNGWVHIMPCCPTIWCQEKLTICGE 555
Db 481 VDGHILKYKEGDIPIHPTNIHKYLVCFFVNGWVHIMPCCPTIWCQEKLTICGE 536

RESULT 6
AAV52533
ID AAV52533 standard; protein; 509 AA.
XX AC AAV52533;
XX DT 06-AUG-2003 (revised)
XX DT 22-FEB-2000 (first entry)
DE D. pteronyssius 98 kD mite allergen protein (map) Pderp98-509.
XX KW Mite allergen protein; map; high molecular weight; HMW-map; allergy;
XX KW house dust mite; IGE; immunoglobulin E; allergen; mapB;
XX KW hypersensitivity reaction; therapy; treatment; diagnosis; human; feline;
XX KW canine; veterinary; antibody; vaccine; immunisation.
XX OS Dermatophagoides pteronyssinus.
XX FH Key Location/Qualifiers
FT Peptide 1..19
FT Protein /note= "Signal peptide"
FT Protein 20..509
FT Protein /note= "Mature Pderp98-509"
XX W09954349-A2.
XX PD 28-OCT-1999.
XX PF 16-APR-1999; 99WO-US008524.
XX PR 17-APR-1998; 98US-00062013.
XX PR 13-MAY-1998; 98US-00852952.
XX PR 02-SEP-1998; 98US-0098909P.
XX PA (HESK-) HESKA CORP.
XX PI McCall CA, Hunter SW, Weber ER;
XX DR WPI; 2000-052700/04.
XX DR N-PSDB; AAZ38585, AAZ38586, AAZ38587, AAZ38588.
XX PT Novel high molecular weight Dermatophagoides nucleic acid polypeptides
XX PT used to modify an animals' hypersensitivity to mite allergens.
XX PS Claim 3; Page 134-136; 154pp; English.
XX CC This sequence represents Dermatophagoides pteronyssius mite allergen
XX CC protein (map) Pderp98-509. Pderp98-509 has a molecular weight of 98 kD,
XX CC comprising 509 amino acids, and has a high degree of homology with the D.
XX CC farinae 98 kD allergen, mapB (AAV52523). Nucleic acid molecules encoding
XX CC Pderp98-509 were isolated from a D. pteronyssius cDNA library by
XX CC hybridisation with a probe encoding the D. farinae high molecular weight
XX CC map (HMW-map) composition. Mite allergenic proteins and peptides, and
XX CC nucleic acids encoding them, may be used in therapeutic compositions to

CC modify an animal's hypersensitivity reaction to mite allergens. Animals
CC that may be treated include mammals and birds, especially felines, canines,
CC equines, humans, other pets, and work or domestic animals. The proteins or
CC fragments may also be used to diagnose allergies via a skin test. The proteins
CC and peptides can also be used to raise antibodies, which have a variety of
CC potential uses. For example, they can be used as vaccines to passively
CC immunise animals against dust mite hypersensitivity, as positive
CC controls in test kits and as tools to recover desired dust mite
CC allergens from a mixture of proteins. (Updated on 06-AUG-2003 to correct OS field.)
XX Sequence 509 AA;
SQ

Query Match 81.8%; Score 2542; DB 3; Length 509;
Best Local Similarity 81.7%; Pred. No. 2e-176;
Matches 456; Conservative 24; Mismatches 26; Indels 52; Gaps 2;
Qy 1 MKTIYAILSIACIGLMAASIKRDHNDYKQPMRIVCYGTWVYHKVDPTTIEDIDPFK 60
Db 1 MKTTFALFCIWACIGLMAAATKRDHNNYSKNPMRIVCYGTWVYHKVDPTTIEDIDPFK 60
Qy 61 CTHLMYGFADKIDYKTIQVDFDYQDDNHNHSEKRGYERFNNLRKLNKPELTMTISLGWY 120
Db 61 CTHLMYGFADKIDYKTIQVDFDYQDDNHNHSEKRGYERFNNLRKLNKPELTMTISLGWY 120
Qy 121 EGSEKYSDMAANPTYRQOFIQSVLDFLOEYKFDGLDLDWEYFGSRLGNPKIDKQNYLALV 180
Db 121 EGSEKYSDMAANPTYRQOFVQSVLDFLOEYKFDGLDLDWEYFGSRLGNPKIDKQNYLTV 180
Qy 181 RELKDAFPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWNNVMTYDHHGWNENFYGHNA 240
Db 181 RELKEAFEPFGYLLTAAVSPGKDKIDVAYELKELNQLFDWNNVMTYDHHGWNENFYGHNA 240
Qy 241 PLYKRPDETDLHTYFNVTYTHYLLNNGATRDKLVMGVPFYGRAWSIEDRSKVLGDPA 300
Db 241 PLYKRPDETDLHTYFNVTYTHYLLNNGATRDKLVMGVPFYGRAWSIEDRSKVLGDPA 300
Qy 301 KGMSPPGFTSGEGVLSYIELCOLFQKEBWHIQDEYNNAPYGYNDKIWGVYDDIASISC 360
Db 301 KGMSPPGFTSGEGVLSYIELCOLFQKEBWHIQDEYNNAPYGYNDKIWGVYDDIASISC 360
Qy 361 KLAFKELGVSQVWWSLENDDFKHCQKPNLLKVNHWINGDEKNSPECILGSPSTTPT 420
Db 361 KLAFKELGVSQVWWSLENDDFKHCQKPNLLKVNHWINGDEKNSPECILGSPSTTPT 420
Qy 421 TPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTT 480
Db 421 TPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTT 434
Qy 481 TPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTT 537
Db 435 ---PTTDTSTSETPKYTTIDGHILKYKQGYLPHTDVKHLYLVCYEYIATFNGGWWHIM 491
Qy 538 PCPRTIWCQEKLTICGE 555
Db 492 DCPKGRWHATLKNKCIQE 509

RESULT 7
AAU96337
ID AAU96337 standard; protein; 509 AA.
XX AC AAU96337;
XX DT 15-JUL-2002 (first entry)
XX DE Der HMW-map polypeptide #24.
XX KW Der HMW-map; American house dust mite; antiallergic; mite; IGE;
XX KW mite allergenic protein; immunoglobulin E; hypersensitivity;
XX KW immunocomplex formation.
XX OS Dermatophagoides farinae.

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XX W0200222807-A2.
XX
XX
XX PD 21-MAR-2002.
XX
XX PF 14-SEP-2001; 2001WO-US028730.
XX
XX PR 14-SEP-2000; 2000US-006622293.
XX
XX PA (HESK-) HESKA CORP.
XX
XX PI McCall CA, Hunter SW, Weber ER;
XX
XX DR WPI; 2002-351888/38.
XX
XX DR N-PSDB; ABK69581.
XX
XX PT New mite allergenic protein isolated from Dermatophagoides, designated
XX Der HW-map protein, useful as a vaccine for treating mite allergy.
XX
XX PS Claim 12; Page 134-136; 161pp; English.
XX
XX CC The invention relates to an isolated mite allergenic protein of
XX Dermatophagoides, designated Der HW-map protein, and its related nucleic
XX acid. The Der HW-map protein is useful for eliciting an immune response
XX against Der HW-map protein. The protein or a reagent comprising a non-
XX proteinaceous epitope is useful for identifying an animal (e.g., dog,
XX cat) susceptible to or having an allergic response to a mite. A
XX therapeutic composition is useful for desensitizing a host animal to an
XX allergic response to a mite. The DNA and protein can be used in the
XX detection of anti-Der HW-map antibodies in animal fluids, and inhibition
XX of immunoglobulin (Ig) E or Der HW-map protein activity associated with a
XX disease. Antibodies that bind to Der HW-map are useful for inhibiting
XX binding of proteins to IgE, to prevent immunocomplex formation, thus
XX reducing hypersensitivity responses to mite allergens, and as vaccines
XX against mite allergen hypersensitivity. Sequences AAU96314-AAU96342
XX represent Der HW-map polypeptides of the invention
XX
XX SQ Sequence 509 AA;
XX
XX Query Match 81.8%; Score 2542; DB 5; Length 509;
XX Best Local Similarity 81.7%; Pred. No. 2e-176;
XX Matches 456; Conservative 24; Mismatches 26; Indels 52; Gaps 2;
XX
XX QY 1 MKTIYAILSIMACIGLGNASIKRDHNDYSKNPMRIVCVGTWVSVYHKVDPTIEDIDPFK 60
XX DB 1 MKTTFALFCIWACIGLGNAAATKRDHNNYSKNPMRIVCVGTWVSVYHKVDPTIEDIDPFK 60
XX
XX QY 61 CTHLMYGFADIKYKTIQVDPYQDDNHNHSEKRGYERFNNLRKNPELTMTISLGGWY 120
XX DB 61 CTHLMYGFADIKYKTIQVDPYQDDNHNHSEKRGYERFNNLRKNPELTMTISLGGWY 120
XX
XX QY 121 EGSEKYSMAANPTVROQFIQSVDLFLOEYKFDGLDLDWEYVPSGRLGNPKIDKQNYLALV 180
XX DB 121 EGSEKYSMAANPTVROQFVSQVSLDFLOEYKFDGLDLDWEYVPSGRLGNPKIDKQNYLTLV 180
XX
XX QY 181 RELKDAFEPHGYLLTAAYSPGKIDRAYDIKELNKLFDWNNVTYDVGHWENFYGHNA 240
XX DB 181 RELKEAFEPFGYLLTAAYSPGKIDRAYELKELNQLFDWNNVTYDVGHWENFYGHNA 240
XX
XX QY 241 PLYKPEPDETLHTYFNNTYTHYLLNNGATRDKLVMGVPPYGRAWSIEDRSKLGDPGA 300
XX DB 241 PLYKPEPDETLHTYFNNTYTHYLLNNGATRDKLVMGVPPYGRAWSIEDRSKLGDPGA 300
XX
XX QY 301 KGMSPFGFISGEGVLSYIELCQLFQKEWHIQDYDEYNNAPYVNDKIWGYDGLASISC 360
XX DB 301 KGMSPFGFITGEGVLSYIELCQLFQKEWHIQDYDEYNNAPYVNDKIWGYDGLASISC 360
XX
XX QY 361 KLAFLKEIGVSWMTWSIENDDPKCHGCPKPKPLLNKVNMMINGEKNSFECLGPSSTTP 420
XX DB 361 KLAFLKEIGVSWMTWSIENDDPKCHGCPKPKPLLNKVNMMINGEKNSFECLGPSSTTP 420
XX
XX QY 421 TPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPT 480
XX
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DB 421 TPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPT 434
QY 481 TSPPTTHTSETPKYTYIVDGHILKCYKEGDIPTHTNIHKYLVCFV---NGGWWVHIM 537
DB 435 ---PTTDTSTSETPKYTYIVDGHILKCYKQGYLPHTDVHKYLVCEYIATPNGGWWVHIM 491
QY 538 PCPPGTIWCQEKLTGICE 555
DB 492 DCPKGTTRWHTLKNCLQE 509
RESULT 8
AAU96338
ID AAU96338 standard; protein; 509 AA.
XX
XX AC AAU96338;
XX
XX DT 15-JUL-2002 (first entry)
XX
XX DE Der HW-map polypeptide #25.
XX
XX KW Der HW-map; American house dust mite; anti-allergic; mite; IgE;
XX mite allergenic protein; immunoglobulin E; hypersensitivity;
XX immunocomplex formation.
XX
XX OS Dermatophagoides farinae.
XX
XX PN W0200222807-A2.
XX
XX PD 21-MAR-2002.
XX
XX PF 14-SEP-2001; 2001WO-US028730.
XX
XX PR 14-SEP-2000; 2000US-006622293.
XX
XX PA (HESK-) HESKA CORP.
XX
XX PI McCall CA, Hunter SW, Weber ER;
XX
XX DR WPI; 2002-351888/38.
XX
XX DR N-PSDB; ABK69583.
XX
XX PT New mite allergenic protein isolated from Dermatophagoides, designated
XX Der HW-map protein, useful as a vaccine for treating mite allergy.
XX
XX PS Claim 12; Page 139-141; 161pp; English.
XX
XX CC The invention relates to an isolated mite allergenic protein of
XX Dermatophagoides, designated Der HW-map protein, and its related nucleic
XX acid. The Der HW-map protein is useful for eliciting an immune response
XX against Der HW-map protein. The protein or a reagent comprising a non-
XX proteinaceous epitope is useful for identifying an animal (e.g., dog,
XX cat) susceptible to or having an allergic response to a mite. A
XX therapeutic composition is useful for desensitizing a host animal to an
XX allergic response to a mite. The DNA and protein can be used in the
XX detection of anti-Der HW-map antibodies in animal fluids, and inhibition
XX of immunoglobulin (Ig) E or Der HW-map protein activity associated with a
XX disease. Antibodies that bind to Der HW-map are useful for inhibiting
XX binding of proteins to IgE, to prevent immunocomplex formation, thus
XX reducing hypersensitivity responses to mite allergens, and as vaccines
XX against mite allergen hypersensitivity. Sequences AAU96314-AAU96342
XX represent Der HW-map polypeptides of the invention
XX
XX SQ Sequence 509 AA;
XX
XX Query Match 81.8%; Score 2542; DB 5; Length 509;
XX Best Local Similarity 81.7%; Pred. No. 2e-176;
XX Matches 456; Conservative 24; Mismatches 26; Indels 52; Gaps 2;
XX
XX QY 1 MKTIYAILSIMACIGLGNASIKRDHNDYSKNPMRIVCVGTWVSVYHKVDPTIEDIDPFK 60
XX DB 1 MKTTFALFCIWACIGLGNAAATKRDHNNYSKNPMRIVCVGTWVSVYHKVDPTIEDIDPFK 60
```


QY 61 CTHLMYGFPAKIDBYKTYIQVDFPYQDDNHNSEKRGYERFNNLRNLKKNPELTMTISLGGWY 120
 DB 61 CTHLMYGFPAKIDBYKTYIQVDFPYQDDNHNSEKRGYERFNNLRNLKKNPELTMTISLGGWY 120
 QY 121 EGSEKYSMAANPTYQOQFQVQVLDLFLQYKFDGLDWEYFGSRLGNPKIDKQNYLTV 180
 DB 121 EGSEKYSMAANPTYQOQFQVQVLDLFLQYKFDGLDWEYFGSRLGNPKIDKQNYLTV 180
 QY 181 RELKDAPEPHGYLLTAASPGKIDRAYDIKELNKLFDWMNVMTYDYGWENFYGHNA 240
 DB 181 RELKEAFEPFGYLLTAASPGKIDVAVELKELNQLFDWMNVMTYDYGWENFYGHNA 240
 QY 241 PLYKRDETDDELTYFNVTMYHYLLNNGATRDKLVMGVPPFYGRAWSIEDRSKLGIDPA 300
 DB 241 PLYKRDETDDELTYFNVTMYHYLLNNGATRDKLVMGVPPFYGRAWSIEDRSKLGIDPA 300
 QY 301 KGMSPGFTSGEGLVSYIELCOLFOKEEWHIQYDEYNNAPYGYNDKIWGVDDDLASISC 360
 DB 301 KGMSPGFTSGEGLVSYIELCOLFOKEEWHIQYDEYNNAPYGYNDKIWGVDDDLASISC 360
 QY 361 KLAFLKELGVGMVMSLENDPKHCGKPKPLNKNVHNMINGDEKNSPECILGSGTTP 420
 DB 361 KLAFLKELGVGMVMSLENDPKHCGKPKPLNKNVHNMINGDEKNSPECILGSGTTP 420
 QY 421 TPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTT 480
 DB 421 TPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTT 480
 QY 481 TPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTT 537
 DB 435 ---PTTDTSTSETPKYTTIDGHLIKCYKQGYLPHPTDVHKLVCBYIATPNGGWWHIM 491
 QY 538 PCPPGTIWQEKUTCIGE 555
 DB 492 DCPKGRWHTATLKNCIQE 509

RESULT 9

AAV52535
 ID RAY52535 standard; protein; 490 AA.
 XX
 AC AAV52535;
 XX
 DT 06-AUG-2003 (revised)
 DT 22-FEB-2000 (first entry)
 XX
 DE D. pteronyssius 98 kD mite allergen protein (map) pDerp98-490.
 XX
 KW Mite allergen protein; map; high molecular weight; HMW-map; allergy;
 KW house dust mite; IgE; immunoglobulin E; allergen; mapB;
 KW hypersensitivity reaction; therapy; treatment; diagnosis; human; feline;
 KW canine; veterinary; antibody; vaccine; immunisation.
 XX
 OS Dermatophagoides pteronyssinus.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 115..117
 FT /note= "Asn is N-glycosylated"
 FT Modified-site 240..242
 FT /note= "Asn is N-glycosylated"
 XX
 PN W09954349-A2.
 XX
 PD 28-OCT-1999.
 XX
 PF 16-APR-1999; 99WO-US008524.
 XX
 PR 17-APR-1998; 98US-00062013.
 PR 13-MAY-1998; 98US-0085295P.
 PR 02-SEP-1998; 98US-0098909P.
 XX
 PA (HESK-) HESKA CORP.
 XX

PI McCall CA, Hunter SW, Weber ER;
 XX WPI; 2000-052700/04.
 DR N-PSDB; AAZ38589, AAZ38590.
 XX Novel high molecular weight Dermatophagoides nucleic acid polypeptides
 PT used to modify an animals' hypersensitivity to mite allergens.
 XX
 PS Claim 3; Page 147-149; 154pp; English.
 CC This sequence represents Dermatophagoides pteronyssius mite allergen
 CC protein (map) pDerp98-490, the mature form of pDerp98-509. pDerp98-490
 CC has a molecular weight of 98 kD, comprising 490 amino acids, and has a
 CC high degree of homology with the D. farinae mature 98 kD allergen, mapB
 CC (AAV52525). Nucleic acid molecules encoding pDerp98-490 were isolated
 CC from a D. pteronyssius cDNA library by hybridisation with a probe
 CC encoding the D. farinae high molecular weight map (HMW-map) composition.
 CC Mite allergenic proteins and peptides, and nucleic acids encoding them,
 CC may be used in therapeutic compositions to modify an animal's
 CC hypersensitivity reaction to mite allergens. Animals that may be treated
 CC include mammals and birds, especially felines, canines, equines, humans,
 CC other pets, and work or domestic animals. The proteins or fragments may
 CC also be used to diagnose allergies via a skin test. The proteins and
 CC peptides can also be used to raise antibodies, which have a variety of
 CC potential uses. For example, they can be used as vaccines to passively
 CC immunise animals against dust mite hypersensitivity, as positive controls
 CC in test kits and as tools to recover desired dust mite allergens from a
 CC mixture of proteins. (Updated on 06-AUG-2003 to correct OS field.)
 XX
 SQ Sequence 490 AA;

Query Match 79.7%; Score 2475; DB 3; Length 490;

Best Local Similarity 82.5%; Pred. No. 1.5e-171;

Matches 443; Conservative 21; Mismatches 21; Indels 52; Gaps 2;

QY 22 KRDNYSKNPMRIVCYVGTWSVYHKVDPTYIEDIDPFKTHLMYGAKEIDYKTYQVF 81
 DB 3 KRDNYSKNPMRIVCYVGTWSVYHKVDPTYIEDIDPFKTHLMYGAKEIDYKTYQVF 62
 QY 82 DPYQDDNHNSEKRGYERFNNLRNLKKNPELTMTISLGGWYEGSEKYSMAANPTYQOQFIQ 141
 DB 63 DPFQDDNHNSEKRGYERFNNLRNLKKNPELTMTISLGGWYEGSEKYSMAANPTYQOQFVQ 122
 QY 142 SVLDPLQYKFDGLDWEYFGSRLGNPKIDKQNYLTVRELKDAPEPHGYLLTAASVSPG 201
 DB 123 SVLDPLQYKFDGLDWEYFGSRLGNPKIDKQNYLTVRELKDAPEPHGYLLTAASVSPG 182
 QY 202 KDKIDRAYDIKELNKLFDWMNVMTYDYGWENFYGHNAPLYKBPDETDDELTYFNVTY 261
 DB 183 KDKIDVAYELKELNQLFDWMNVMTYDYGWENFYGHNAPLYKBPDETDDELTYFNVTY 242
 QY 262 MHYLLNNGATRDKLVMGVPPFYGRAWSIEDRSKLGIDPAKGMSPGFTSGEGLVSYIEL 321
 DB 243 MHYLLNNGATRDKLVMGVPPFYGRAWSIEDRSKLGIDPAKGMSPGFTSGEGLVSYIEL 302
 QY 322 COLFOKEEWHIQYDEYNNAPYGYNDKIWGVDDDLASISCKLAFKELGVGMVMSLEND 381
 DB 303 COLFOKEEWHIQYDEYNNAPYGYNDKIWGVDDDLASISCKLAFKELGVGMVMSLEND 362
 QY 382 DFKHCGKPKPLNKNVHNMINGDEKNSPECILGSGTTPPTTPTTPTTPTTPTTPTTPTT 441
 DB 363 DFKHCGKPKPLNKNVHNMINGDEKNSPECILGSGTTPPTTPTTPTTPTTPTTPTTPTT 415
 QY 442 TPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTT 501
 DB 416 -----PTTDTSTSETPKYTYID 433
 QY 502 GHLIKCYKEGDIHPHTNIHKYLVCBEFV---NGGWWHIMPCPPGTIWQEKUTCIGE 555
 DB 434 GHLIKCYKQGYLPHPTDVHKLVCBYIATPNGGWWHIMDCPKGRWHTATLKNCIQE 490

RESULT 10

AAU96339
ID AAU96339 standard; protein; 490 AA.
XX AC
XX AAU96339;
XX DT 15-JUL-2002 (first entry)
XX DE Der HMW-map polypeptide #26.
XX KW Der HMW-map; American house dust mite; antiallergic; mite; IgE;
XX KW mite allergenic protein; immunoglobulin E; hypersensitivity;
XX KW immunocomplex formation.
XX OS Dermatophagoides farinae.
XX PN WO200222807-A2.
XX PD 21-MAR-2002.
XX PF 14-SEP-2001; 2001WO-US028730.
XX PR 14-SEP-2000; 2000US-00662293.
XX PA (HESK-) HESKA CORP.
XX PI McCall CA, Hunter SW, Weber ER;
XX DR WPI; 2002-351888/38.
XX DR N-PSDB; ABK69585.
XX PT New mite allergenic protein isolated from Dermatophagoides, designated
XX PT Der HMW-map protein, useful as a vaccine for treating mite allergy.
XX PS Claim 12; Page 144-146; 161pp; English.
XX CC The invention relates to an isolated mite allergenic protein of
XX CC Dermatophagoides, designated Der HMW-map protein, and its related nucleic
XX CC acid. The Der HMW-map protein is useful for eliciting an immune response
XX CC against Der HMW-map protein. The protein or a reagent comprising a non-
XX CC proteinaceous epitope is useful for identifying an animal (e.g., dog,
XX CC cat) susceptible to or having an allergic response to a mite. A
XX CC therapeutic composition is useful for desensitising a host animal to an
XX CC allergic response to a mite. The DNA and protein can be used in the
XX CC detection of anti-Der HMW-map antibodies in animal fluids, and inhibition
XX CC of immunoglobulin (Ig)E or Der HMW-map protein activity associated with a
XX CC disease. Antibodies that bind to Der HMW-map are useful for inhibiting
XX CC binding of proteins to IgE, to prevent immunocomplex formation, thus
XX CC reducing hypersensitivity responses to mite allergens, and as vaccines
XX CC against mite allergen hypersensitivity. Sequences AAU96314-AAU96342
XX CC represent Der HMW-map polypeptides of the invention
XX SQ Sequence 490 AA;
Query Match 79.7%; Score 2475; DB 5; Length 490;
Best Local Similarity 82.5%; Pred. No. 1.5e-171;
Matches 443; Conservative 21; Mismatches 21; Indels 52; Gaps 2;
QY 22 KRDHNDYKSNRIVCYVGTWSVHKVDPYTIEDIDPKCTHLMYGAKIDYKTIQVF 81
Db 3 KRDHNYKSNRIVCYVGTWSVHKVDPYTIEDIDPKCTHLMYGAKIDYKTIQVF 62
QY 82 DPYQDDNNSWEKRGYERFNNLRKNPELTMTISLGWYEGSEKYSDMAANPTYRQOFIQ 141
Db 63 DPYQDDNNSWEKRGYERFNNLRKNPELTMTISLGWYEGSEKYSDMAANPTYRQOFVQ 122
QY 142 SVLDPLQYKFGDLDDWEYFGSRLGNPKIDKQNYLALVRELKDAFEPHYLLTAASVPG 201
Db 123 SVLDPLQYKFGDLDDWEYFGSRLGNPKIDKQNYLALVRELKDAFEPHYLLTAASVPG 182
QY 202 KDKIDRAVDIKELNKLFDWMNVMTYDYGCHWFNFGHNAPLYKRPDETDLHTYFNVT 261
Db 183 KDKIDRAVDIKELNKLFDWMNVMTYDYGCHWFNFGHNAPLYKRPDETDLHTYFNVT 242

262 MHYLLNNGATRDKLVMGVPFFYGRANSIEDRSKILGDPAGKMSPPGFTSGEGVLSYIEL 321
243 MHYLLNNGATRDKLVMGVPFFYGRANSIEDRSKVLGDPAGKMSPPGFTSGEGVLSYIEL 302
322 CQLFQKEWHIQYDEYNAPYGYNDKIWGVYDDLASISCKLAFLKELGVSQVWWSLEND 381
303 CQLFQKEWHIQYDEYNAPYGYNDKIWGVYDDLASISCKLAFLKELGVSQVWWSLEND 362
382 DFKHGCGPKNPLLNKVHNMINGDEKNSPECILGPSTTTPTPTTTTPTTTTPTTPTTPTT 441
363 DFKHGCGPKYPLLNKVHNMINGDEKNSYECLLGPGSTTTPTPTTPTTPTTPTTPTTPTT 415
442 TTTPTPTPTTTPT 501
416 -----PTTDTSETPKYTYID 433
502 GHLIKYKEGDIPHPTNIHKYLVCFV---NGGWVHIMPCPGTGWQEKUTCTIGE 555
434 GHLIKYKQGYLPHTDVKHLYVCEYIATPNGGWVHIMDCPKGRWHATLKNCIQE 490

RESULT 11
ABP72636
ID ABP72636 standard; protein; 525 AA.
XX AC
XX ABP72636;
XX DT 11-JUN-2003 (first entry)
XX DE Anopheles gambiae chitinase.
XX KW Insecticide; pesticide; insect control; insect; toxin; chitinase; enzyme;
XX KW neuropeptide; transgenic plant; crop protection; mosquito.
XX OS Anopheles gambiae.
XX PH Key Location/Qualifiers
XX FT Peptide 1..19
XX FT Protein /label= Signal_peptide
XX FT /label= Mature_protein
XX FT Misc-difference 31
XX FT /note= "possible trypsin activation site"
XX FT Misc-difference 32
XX FT /note= "possible trypsin activation site"
XX FT Active-site 150..157
XX FT Domain 401..466
XX FT /note= "serine/threonine/proline-rich domain"
XX PN WO2003014150-A2.
XX PD 20-FEB-2003.
XX PF 06-AUG-2002; 2002WO-GB003596.
XX PR 08-AUG-2001; 2001GB-00019274.
XX PA (UYDU-) UNIV DURHAM.
XX PA (ENVI-) DEPT ENVIRONMENT FOOD & RURAL AFFAIRS.
XX PI Gatehouse JA, Fitches EC, Edwards JP;
XX DR WPI; 2003-278469/27.
XX DR N-PSDB; ABZ81875.
XX PT Fusion protein useful for combating insect pests, comprises a
XX PT translocating moiety comprising a plant protein capable of acting as a
XX PT carrier to translocate toxic moiety inside plant pathogen, and a toxic
XX PT moiety.
XX PS Claim 7; Fig 15; 51pp; English.
XX CC The present sequence is that of the mosquito Anopheles gambiae chitinase.

CC This protein is used in claimed fusion proteins of the invention. Such
 CC fusion proteins comprise a translocating moiety and a toxic moiety, where
 CC the translocating moiety is a plant protein (e.g. a lectin) capable of
 CC acting as a carrier to translocate the toxic moiety across the gut wall
 CC of a plant pathogen, and the toxic moiety is an insect-derived peptide or
 CC protein capable of causing deleterious effects on growth, development,
 CC reproduction or mortality in pest insects. Suitable insect peptides and
 CC proteins include allatostatins, chitinase, diuretic hormone and their
 CC metabolites and analogues. Polynucleotides encoding the fusion protein,
 CC vectors, host cells and transgenic plants that are resistant to disease
 CC degradation in the insect gut
 XX
 SQ Sequence 525 AA;

Query Match 32.5%; Score 1008.5; DB 6; Length 525;
 Best Local Similarity 38.4%; Pred. No. 7.7e-65;
 Matches 211; Conservative 93; Mismatches 187; Indels 59; Gaps 13;

QY 8 LSIACIGLNASIKRD-HNDYSKNPMRIVCVYVTSVYHKVD-PYTIEDIPFKCTHLM 65
 Db 5 VGVLLVIAAFAAEHKAASAEKGVYVYVGTVAVRPGNGRYDIEHIDPSLCTHLM 64
 QY 66 YGFAKIDVYKTIQVDPYQDDNHNHNSWEKRGYERFNNLRKKNPELTTMISLGGWYEGSEK 125
 Db 65 YGFFGINE-DATVRIIDPVLDEEN-WGRGHKRFVGLKNVGPGLKTLAAIGWEGSRK 122
 QY 126 YSDMAANPTVROQFIQSVLDFLOEYKFDGLDLDWEYFGSLRGKPKIDKQNLALVRELKD 185
 Db 123 FSAMAASGELRKFI SDCAVFCQHGFDGLDLDWEYPAQDGNPLIDRDHNAQLVEEMRE 182
 QY 186 APFPHGYLTAASVPGKIDRAYDIKELNKLPDMNVNTYDVGWENFYGHNAPLYKR 245
 Db 183 EFDHYGLLTAASVAFSGVSYDIPRISKSFHFLNMVYDMHGAWDSYCGINAPLYRG 242
 QY 246 PDETDELTFYFNNTYTHYLLNNGATRDKLVMGVPPYFGRAWSDIESKLGDPKAGMSP 305
 Db 243 SADTDLRGQINVASIHFWLAQGGCTGRKLVGLIPLYGRNFTLASAANTQIGAPTGGGT 302
 QY 306 PGFISEEGVLSYIELCOLFQKEWHIOYDEVYNAFYNDKLVGYDDLASICKLAF 365
 Db 303 VGYRTREPGVMGNECEKATEADLRWSEQQVYAVRNQWVGYYDLDLSVQLKVKYL 362
 QY 366 KELGSGVMVWSLENDDFKHC-GPKNPLLNKVNMMINGDEKNSFECILGPSTPTPTT 424
 Db 363 LQGLGAMVWSLETD DFLGCGGGRYPLMHEIRSLVNGT-----PSTTTPSV 413
 QY 425 TPT 484
 Db 414 APTT-----STVAPGTTTTTTCANEGTTQPPT--SDAPNHTTSTTEGNGPTTRPSPG 466
 QY 485 TTEHTSETPKYTYVDGHLIKCY--KEGDIHPHTNHHKYLVC-----EFVNGGWWH 535
 Db 467 -----DG---PCAGGRYGFVPHPTNCARYYICLTADTYEFT----- 500
 QY 536 IMPCPPGTIW 545
 Db 501 ---CPPTILP 507

RESULT 12

ABBS58595
 ID ABB58595 standard; protein; 4498 AA.

XX ABB58595;

AC ABB58595;

XX 26-MAR-2002 (first entry)

XX Drosophila melanogaster polypeptide SEQ ID NO 2577.

XX Drosophila; developmental biology; cell signalling; insecticide;
 XX pharmaceutical.

OS Drosophila melanogaster.

XX WO200171042-A2.

XX 27-SEP-2001.

XX 23-MAR-2001; 2001WO-US009231.

XX 23-MAR-2000; 2000US-0191637P.

XX 11-JUL-2000; 2000US-00614150.

XX (PEKE) PE CORP NY.

XX Venter JC, Adams M, Li PWD, Myers EW;

XX WPI; 2001-656860/75.

XX N-PSDB; ABL02698.

PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signaling and cell-cell
 PT interactions.

PS Disclosure; SEQ ID NO 2577; 21pp + Sequence Listing; English.

CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (AB116176-AB130511), expressed DNA
 CC sequences (AB101840-AB116175) and the encoded proteins (ABBS7737-
 CC ABB72072). The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 4498 AA;

Query Match 27.5%; Score 854.5; DB 4; Length 4498;
 Best Local Similarity 33.8%; Pred. No. 2e-52;
 Matches 202; Conservative 88; Mismatches 188; Indels 119; Gaps 21;

QY 2 KTIYALISVACIGLGNASIKRDHNDYSKNPMRIVCVYVTSVYH-----KVDPTTIEDID 57
 Db 33 QTLFLCALAYCI-----NEASSEG-RVVCYVYVTSVYRPGTAKFNP---QNIN 77
 QY 58 PFKCTHLMY---GFAKIDVYKTIQVDPYQDDNHNHNSWEKRGYERFNNLRKKNPELTTMI 114
 Db 78 PYLCTHLYAFAGGFTKDNQMK---PFDKYQD-----IEQGYAKFTGLKTYNKQLKTI 128
 QY 115 SLGGWYEGSEKYSDMAANPTVROQFIQSVLDFLOEYKFDGLDLDWEYFGSLRGKPKIDKQ 174
 Db 129 AIGWNASRSPSLVASNERRQOFIKNILKFLQNHFDGIDLDWEYPAHREGSKSRDRD 188
 QY 175 NYLALVRELKDAFPHFG-----YLLTAASVPGKIDRAYDIKELNKLPDMNVNTYD 227
 Db 189 NYAQVQELRAEFERAEKTRTELLTMAVPAGIEYDKGYDVPKLYLDWENLVLYD 248
 QY 228 YHGWENFYGHNAPLYKRPDETDELTY---FNVNTYTHYLLNNGATRDKLVMGVPPYGR 284
 Db 249 FHSSHEPSVNHAPLYSL--EEDSEVNYDAELNIDYSIKYLLKAGADRDKLVLDIPTYGR 306
 QY 285 AWSIEDRSKLGDPKAGMSPPGFISGEEVLSYIELCOLFQKE-EWH-IQYDEVYVNA 342
 Db 307 SYTLNEESTELGAPAGPGEGQGDATREKGYLAYEICQLKDDPEVTVVQPNANVNGPY 366
 QY 343 GYNDKIWVGYYDDLASICKLAFKELGVSGVWWSLENDDFKHC-GPKNPLLNKVNMI 401
 Db 367 AYRNQWVGYYDDLAIVRKAEYVVAQGLGIMFWAINDDDFRGTCNCKPPLIEAA---- 422
 QY 402 NGDKNSFECILGPSTPT 445
 Db 423 ---KEAWVEALGLGINEVAKFSGPQKPSRSRSDNASNRLNKGKTEAPLSSRRPSATR 478

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QY 446 STPTPTPTPTPTPTPTT-----PSTPTPTPTPTPTPTPTPTPTPTPTT 489
Db 479 RPAVSTQAPP--PSTTKFLTEAGSSLYIGGRASTTTPPTPTTDP-----522
QY 490 TSETPKYTYVDGHLIKVCKSGDIPHPNTHKLVLCFVANG---GWWVHMPCPPG 542
Db 523 -----GSDFKCEEEGFFQHPRDCKKYWC-LDSGSGLGIVAHMFTCPSG 566

RESULT 13
AAW01824
ID AAW01824 standard; protein; 554 AA.
AC XX
AC AAW01824;
XX XX
DT 27-MAY-1997 (first entry)
XX XX
DE Manduca sexta larva epidermal and gut chitinase.
XX XX
KW Chitinase; insect; transgenic plant; biological control; baculovirus;
KW biocide; insecticide; tobacco hookworm.
XX XX
OS Manduca sexta.
XX XX
FH Key Location/Qualifiers
FT Peptide 1..19
FT FT /label= Sig_peptide
FT Protein 20..554
FT FT /label= Mat_protein
FT Region 97..111
FT FT /label= Conserved_region-I
FT FT Active-site 136..148
FT FT /note= "proposed active site"
XX XX
PN W09708944-A1.
XX XX
XX 13-MAR-1997.
XX XX
XX 06-SEP-1996; 96WO-US014440.
XX XX
XX 06-SEP-1995; 95US-00524051.
XX XX
XX (UNIV ) UNIV KANSAS STATE RES FOUND.
XX XX
XX Kramer KJ, Muthukrishnan S, Choi HK, Corpuz L, Gopalakrishnan B;
XX WPI; 1997-192586/17.
XX N-PSDB; AAT62557.
XX XX
XX Transgenic plant contg. recombinant insect chitinase coding sequence -
XX useful for controlling plant pests.
XX XX
XX Claim 4; Page 37-40; 57pp; English.
XX XX
XX An epidermal and gut chitinase (AAW01824) of Manduca sexta is encoded by
XX cDNA clone 201 (AAT62557), isolated from a day-6 fifth instar whole larva
XX cDNA library. The cDNA can be inserted into a vector for host expression
XX of the chitinase protein, and may be utilised to control a population of
XX insect pests. A recombinant baculovirus vector is provided for this
XX purpose, as well as a transgenic tobacco plant that shows increased
XX resistance to tobacco hornworm. Recombinant chitinase may also be
XX expressed in host cells or larvae for subsequent purification and use as
XX a biocide. The insect chitinase is expected to be more potent as an
XX insect control agent than chitinaes from other sources
XX XX
SQ Sequence 554 AA;

Query Match 27.0%; Score 838.5; DB 2; Length 554;
Best Local Similarity 35.4%; Pred. No. 1.9e-52;
Matches 208; Conservative 79; Mismatches 210; Indels 91; Gaps 20
QY 6 AILSINACIGLANNASIKRDNDYSKNPRIVCYVGTMSVHK-VDPYTIIDPFKCTHL 64

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XX PS Disclosure; Col 53-58; 40pp; English.

XX CC The present sequence is the protein sequence for the Manduca sexta gut

CC chitinase. It was used to isolate the Drosophila melanogaster imaginal

CC disc growth factor 4 (IDGF4) coding sequence. IDGF4 is a member of the

CC chitinase related proteins (CHRP) and is involved in the promotion of

CC cell growth, motility and morphogenesis. The gene and protein are

CC expected to have mammalian homologues. They can be used in the treatment

CC of cancer, wound healing, tissue regeneration following arthritis,

CC osteoporosis, other skeletal disorders and burns, for revitalising scar

CC tissue resulting from surgical procedures, irradiation, laceration, toxic

CC chemicals, viral or bacterial infection or burns, to promote tissue

CC growth during tissue engineering, for example tissues for skin graft

CC replacements and bone regrowth, and to modulate the function of the

CC female reproductive tract. In addition, they can also be used to increase

CC meat, egg, sperm and milk production in animals. One possible method of

CC use is by gene therapy

XX SQ Sequence 554 AA;

Query Match 27.0%; Score 838.5; DB 3; Length 554;

Best Local Similarity 35.4%; Pred. NO. 1.9e-52;

Matches 208; Conservative 79; Mismatches 210; Indels 91; Gaps 20;

QY 6 AILSIMACIGLMNASIKRDNDYKSNPMRIVCVGTWMSVYHK-VDPYTIEDIDPFKCTHL 64

Db 3 ATLATLAVLATAV-----QSDSRARIVCFNSWAVYRPGVGRYGIEDIPVEKCTHI 55

QY 65 MYGFAKIDEXKYTIQVFPDQDDNHNSEKRGYERFNRLKKNPELTMTISLGGWYEGSE 124

Db 56 IYSGFIGVTEGSEVLIIDPELD-----VDKNGFRNFTSLRSHSPVKFWAVGGWAGSS 110

QY 125 KYSDMAANPTYRQQTQSVDLDFIOEYKFDGLDWEYFGSR-LGNPKIDKQNYLALVREL 183

Db 111 KYSHWAQKSTRMSFIRSVSFLKKYDFDGLDWEYFGAARDGGSFSDKDKFLYLVOEL 170

QY 184 KDAP--EPHGYLITAAVSPGKIDRAYDIKELKLPDMVNVYTYDYGHWENFYGHNAP 241

Db 171 RRARIRVKGWELTAAPLANFNLMEGYHVPFLCOELDAITHVMSYDLRGNWAGFADVHSP 230

QY 242 LYKRPDETDLHTYFVNYTHYVNLNNGATRDKLVMGVPFYGRAWSIED-----290

Db 231 LYKRPED-QWAYEKLNVNDGLHLWEKGCPSNKLVLVGIPFYGRSFTLSAGNNYGLGTI 289

QY 291 RSKLKGDPKAGMSPPGFISGEGVLSYIELCOLFOKEE--WHIQYDEYVNPAGYNDKI 348

Db 290 NKEAGGDPAPYTNATG-----WAYEICTEVDKDSGWTKKWDEQCKCEYAKGTQ 342

QY 349 WVGYYDLIAS-SCKLAFKELGVSGVMVWVMSLENDDFKHGCGPKXPLNKNVHNMINGDEKNS 408

Db 343 WVGYYDPRSVEIKMWNWKQKYLCAWTWAIMDDDFQGLCGEKPKLIKILHKMS-----396

QY 409 FECILGSTTTPTTPTTPTT-----TTPTPS-----PTPTTPTTPTTPTTPTSP 456

Db 397 -----SYTVPPPHTEHTTPTPEWAPPPTSPDSEGDPIPTTTAKPASITTKTKVT 449

QY 457 TTPTTPTSPPT-----PTP-TTPTAPTSTPTTPTTHTSETPKTYTVVGHLI 505

Db 450 TTTAKPPQSVDENDINVRPKPEPQPEVEVP-PTNEB-----VDGSEI 497

QY 506 KCYKEGDP-IPHTNINIKYLVCFVNGGWWHIMPCPPGTTWCQEKLTIC 552

Db 498 -CNSDQDIYDKKDKCYKWC--VNGE--AMQPSQCQGTGVNVLNVC 540

RESULT 15

ABP72619

ID ABP72619 standard; protein; 554 AA.

XX AC ABP72619;

XX DT 11-JUN-2003 (first entry)

XX DE Manduca sexta chitinase.

XX KW Insecticide; pesticide; insect control; insect; toxin; chitinase; enzyme;

XX KW neuropeptide; transgenic plant; crop protection.

XX OS Manduca sexta.

XX FH Key Location/Qualifiers

FT Peptide 1..19

FT Protein /label= Signal_peptide 20..554

FT Modified-site /label= Mature_protein 85..88

FT Active-site /note= "Asn is N-glycosylated" 138..146

FT Modified-site 303..306

FT Modified-site /note= "Asn is N-glycosylated" 545..548

FT Modified-site /note= "Asn is N-glycosylated"

XX WO2003014150-A2.

XX PD 20-FEB-2003.

XX PF 06-AUG-2002; 2002WO-CB003598.

XX PR 08-AUG-2001; 2001GB-00019274.

XX PA (UYDU-) UNIV DURHAM.

XX PA (ENVI-) DEPT ENVIRONMENT FOOD & RURAL AFFAIRS.

XX PI Gatehouse JA, Fitches EC, Edwards JP;

XX WPI; 2003-278469/27.

XX PT Fusion protein useful for combating insect pests, comprises a

PT translocating moiety comprising a plant protein capable of acting as a

PT carrier to translocate toxic moiety inside plant pathogen, and a toxic

PT moiety.

XX Claim 7; Fig 10; 51pp; English.

CC The present sequence is that of Manduca sexta chitinase. This protein can

CC be used in claimed fusion proteins of the invention. Such fusion proteins

CC comprise a translocating moiety and a toxic moiety, where the

CC translocating moiety is a plant protein (e.g. a lectin) capable of acting

CC as a carrier to translocate the toxic moiety across the gut wall of a

CC plant pathogen, and the toxic moiety is an insect-derived peptide or

CC protein capable of causing deleterious effects on growth, development,

CC reproduction or mortality in pest insects. Suitable insect peptides and

CC proteins include allatostatin, chitinase, diuretic hormone and their

CC metabolites and analogues. Polynucleotides encoding the fusion protein,

CC vectors, host cells and transgenic plants that are resistant to disease

CC are also provided. The fusion protein is target-specific, and resists

CC degradation in the insect gut

XX SQ Sequence 554 AA;

Query Match 27.0%; Score 838.5; DB 6; Length 554;

Best Local Similarity 35.4%; Pred. NO. 1.9e-52;

Matches 208; Conservative 79; Mismatches 210; Indels 91; Gaps 20;

QY 6 AILSIMACIGLMNASIKRDNDYKSNPMRIVCVGTWMSVYHK-VDPYTIEDIDPFKCTHL 64

Db 3 ATLATLAVLATAV-----QSDSRARIVCFNSWAVYRPGVGRYGIEDIPVEKCTHI 55

QY 65 MYGFAKIDEXKYTIQVFPDQDDNHNSEKRGYERFNRLKKNPELTMTISLGGWYEGSE 124

Db 56 IYSGFIGVTEGSEVLIIDPELD-----VDKNGFRNFTSLRSHSPVKFWAVGGWAGSS 110

QY 125 KYSDMAANPTYRQQTQSVDLDFIOEYKFDGLDWEYFGSR-LGNPKIDKQNYLALVREL 183

Db 111 KYSHMVAQKSTRMSFIRSVVSFLKKYDFDGLDLDMWEYFGAADRGGSGFSKDKFELYLVQEL 170
QY 184 KDAF--EPHGYYLTAAYSPGKIDRAYDIDKELNKLFDWNNVNTYDHYHGGWENFYGHNAP 241
Db 171 RRAFIRVGKWEITAAVPLANFRIMEGYHVPFELCQELDAIHVMSYDLRGNWAGFADVHSP 230
QY 242 LYKRPDTEDELHTYFNVNNTMYHYNNGATRDKLVNGVFPFYGRAWSIED----- 290
Db 231 LYKRPHD-QWAYEKLNVNDGLHLWEKGCPSNKLVGIPFYGRSFTLSAGNNNYGLGTFI 289
QY 291 RSKLKLDPAKGMSPPGFISGEGVLSYIELCQLFOKEE--WHIQYDEYNAFYGYNDKI 348
Db 290 NKEAGGDEPAPYTNATG-----WAYYEICTEVDKDDSGWTKWDEQCKCFYAYKGTQ 342
QY 349 WVGYDDLASISCKLAFELKELGVSVMVMSLENDDEFGHCGPKNPLANKVHNMINGDEKNS 408
Db 343 WVGYEDPRSVEIKNNWIKQKGYLGAMTWAIDMDDFQGLCGERNPLIKILHKHVS----- 396
QY 409 FECILGPSTTPTPTTPTPT-----TPTTPS-----PTTPTTPTPTTPTTPTSP 456
Db 397 -----SYIVPPHTENTTPTPEWARPPSTPSDPSEGDPIPTTTAKPASITKTKTKT 449
QY 457 TPTPTTPTPT-----PTP-TTPTAPTSTPTTTEHSETPKYTYVDGHLI 505
Db 450 TTTTAKPPQSVIDEENDINVRPEPKPEPQPEPEVEP-PTENE-----VDGSEI 497
QY 506 KCIYKED-IPHTNIHKYLVCEPVGWGWVHIMPCPGTIWCOEKLTC 552
Db 498 -CNSDQDYIPDKKCDKYWRC--VNGE--AMQFSCQHGTVFNVELNYC 540

Search completed: March 22, 2004, 06:51:45
Job time : 170.752 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 22, 2004, 06:59:34 ; Search time 113.53 Seconds
(without alignments)
1265.926 Million cell updates/sec

Title: US-09-662-293-15

Perfect score: 3107
Sequence: 1 MKTIYAILSIMACIGLNMNAS.....IMPCPPGTINQCKELTIGCE 555

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1049977 seqs, 258955339 residues

Total number of hits satisfying chosen parameters: 1049977

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Published Applications AA:**
- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
 - 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
 - 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
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 - 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
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 - 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
 - 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
 - 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
 - 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3107	100.0	555	14	US-10-218-743-15
2	3107	100.0	555	14	US-10-218-743-18
3	3014	97.0	536	14	US-10-218-743-21
4	2542	81.8	509	14	US-10-218-743-35
5	2542	81.8	509	14	US-10-218-743-38
6	2475	79.7	490	14	US-10-218-743-41
7	738	23.8	445	14	US-10-004-219B-10
8	738	23.8	466	14	US-10-161-547-2
9	736.5	23.7	473	14	US-10-004-219B-4
10	732	23.6	466	14	US-10-161-547-4
11	729.5	23.5	452	14	US-10-004-219B-9
12	721.5	23.2	373	14	US-10-161-547-14
13	721.5	23.2	373	14	US-10-161-547-15
14	708.5	22.8	455	14	US-10-004-219B-14
15	708.5	22.8	476	14	US-10-004-219B-1

16	705.5	22.7	617	15	US-10-369-493-6743	Sequence 6743, Ap
17	668	21.5	678	15	US-10-295-027-632	Sequence 632, App
18	662.5	21.3	457	15	US-10-094-749-1900	Sequence 1900, Ap
19	662	21.3	383	14	US-10-097-340-45	Sequence 45, Appl
20	662	21.3	383	15	US-10-295-027-270	Sequence 270, App
21	650	20.9	383	9	US-09-459-749D-17	Sequence 17, Appl
22	630	20.3	385	15	US-10-295-027-278	Sequence 278, App
23	630	20.3	423	15	US-10-373-802-2	Sequence 2, Appll
24	592	19.1	599	15	US-10-369-493-17162	Sequence 17162, A
25	521.5	16.8	407	15	US-10-369-493-20271	Sequence 20271, A
26	516	16.6	428	15	US-10-369-493-16644	Sequence 16644, A
27	471	15.2	392	15	US-10-369-493-19361	Sequence 19361, A
28	458	14.7	351	15	US-10-369-493-12478	Sequence 12478, A
29	438	14.1	366	12	US-10-424-599-209667	Sequence 209667, A
30	414.5	13.3	485	15	US-10-369-493-3399	Sequence 3399, Ap
31	406	13.1	371	9	US-09-923-844B-2	Sequence 2, Appll
32	405	13.0	546	15	US-10-369-493-18584	Sequence 18584, A
33	401.5	12.9	399	14	US-10-316-754-11	Sequence 11, Appl
34	401.5	12.9	399	14	US-10-316-754-19	Sequence 19, Appl
35	372.5	12.0	449	15	US-10-369-493-3308	Sequence 3308, Ap
36	367.5	11.8	511	15	US-10-369-493-1684	Sequence 1684, Ap
37	352.5	11.3	572	15	US-10-369-493-18585	Sequence 18585, A
38	350.5	11.3	358	12	US-10-425-114-47084	Sequence 47084, A
39	350.5	11.3	365	12	US-10-424-599-273219	Sequence 273219, A
40	347.5	11.2	567	15	US-10-369-493-8158	Sequence 8158, Ap
41	337	10.8	789	15	US-10-369-493-12804	Sequence 12804, A
42	329.5	10.6	445	15	US-10-369-493-3089	Sequence 3089, Ap
43	317.5	10.2	452	15	US-10-369-493-8244	Sequence 8244, Ap
44	314	10.1	432	15	US-10-369-493-5521	Sequence 5521, Ap
45	313.5	10.1	607	14	US-10-156-761-10415	Sequence 10415, A

ALIGNMENTS

RESULT 1

US-10-218-743-15
; Sequence 15, Application US/10218743
; Publication No. US20030096779A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: 2002-08-13
; PRIOR APPLICATION NUMBER: US/10/218,743
; PRIOR FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/09/292,225
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: 60/098,909
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/085,295
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/098,565
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: 09/062,013
; PRIOR FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 555
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-10-218-743-15

Query Match 100.0%; Score 3107; DB 14; Length 555;
Best Local Similarity 100.0%; Pred. No. 3e-220;
Matches 555; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKTIYAILSIMACIGLNMNASIKEDNDYSCNPMRIVCYVGTWVSVYHKVDYTTIEDIDPFK 60
Db 1 MKTIYAILSIMACIGLNMNASIKEDNDYSCNPMRIVCYVGTWVSVYHKVDYTTIEDIDPFK 60

QY 61 CTHLMYGAFAKIDEXKTYIQVDFPDYQDDNHNHNSWEKRGYERFNNLRKNPELTTMISLGGWY 120
DB 61 CTHLMYGAFAKIDEXKTYIQVDFPDYQDDNHNHNSWEKRGYERFNNLRKNPELTTMISLGGWY 120
QY 121 EGSEKYSDMAANPYRQOFIQSVLDFLOEYKFDGLDLDWEYPGSRGKPKIDKQNYLALV 180
DB 121 EGSEKYSDMAANPYRQOFIQSVLDFLOEYKFDGLDLDWEYPGSRGKPKIDKQNYLALV 180
QY 181 RELKDAFEPHGYLLTAAVSPGKOKIDRAYDIKELNKLFDWMNVTYDYHGGWENFYGHNA 240
DB 181 RELKDAFEPHGYLLTAAVSPGKOKIDRAYDIKELNKLFDWMNVTYDYHGGWENFYGHNA 240
QY 241 PLYKRPDETDELHTYFNNVTMYYLNGATRDKLVMGVFPYGRAMSIEDRSKLGDPDA 300
DB 241 PLYKRPDETDELHTYFNNVTMYYLNGATRDKLVMGVFPYGRAMSIEDRSKLGDPDA 300
QY 301 KGMSPPGFISGEGVLSYIELCOLFQKEEWHIOYDEYNNAPYGVNDKIWGYDDLASISC 360
DB 301 KGMSPPGFISGEGVLSYIELCOLFQKEEWHIOYDEYNNAPYGVNDKIWGYDDLASISC 360
QY 361 KLAFLKELGVSGVMVWVWLENDDFKHCQPKNPLLNKVNHNMGDEKNSFECILGPSTTTP 420
DB 361 KLAFLKELGVSGVMVWVWLENDDFKHCQPKNPLLNKVNHNMGDEKNSFECILGPSTTTP 420
QY 421 TPSTTTTHTSETPKYTYVDGHLIKCYKEGDIHPHTNIHKYLVCFVNGWVWHIMPCP 540
DB 421 TPSTTTTHTSETPKYTYVDGHLIKCYKEGDIHPHTNIHKYLVCFVNGWVWHIMPCP 540
QY 541 PGTINWQCEKLTICGE 555
DB 541 PGTINWQCEKLTICGE 555

RESULT 2

US-10-218-743-18
; Sequence 18, Application US/10218743
; Publication No. US20030096779A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/10/218,743
; PRIOR FILING DATE: 2002-08-13
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: 60/098,909
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/085,295
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/098,565
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: 09/062,013
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 18
; LENGTH: 555
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-10-218-743-18

Query Match 100.0%; Score 3107; DB 14; Length 555;
Best Local Similarity 100.0%; Pred. No. 3e-220;
Matches 555; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKTIYAILISMACIGLMNASIKRDHNDYSKNPMRIVCVGTWVSVHKVDPYTIIDIDPFK 60
DB 1 MKTIYAILISMACIGLMNASIKRDHNDYSKNPMRIVCVGTWVSVHKVDPYTIIDIDPFK 60
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DB 61 CTHLMYGAFAKIDEXKTYIQVDFPDYQDDNHNHNSWEKRGYERFNNLRKNPELTTMISLGGWY 120
QY 121 EGSEKYSDMAANPYRQOFIQSVLDFLOEYKFDGLDLDWEYPGSRGKPKIDKQNYLALV 180
DB 121 EGSEKYSDMAANPYRQOFIQSVLDFLOEYKFDGLDLDWEYPGSRGKPKIDKQNYLALV 180
QY 181 RELKDAFEPHGYLLTAAVSPGKOKIDRAYDIKELNKLFDWMNVTYDYHGGWENFYGHNA 240
DB 181 RELKDAFEPHGYLLTAAVSPGKOKIDRAYDIKELNKLFDWMNVTYDYHGGWENFYGHNA 240
QY 241 PLYKRPDETDELHTYFNNVTMYYLNGATRDKLVMGVFPYGRAMSIEDRSKLGDPDA 300
DB 241 PLYKRPDETDELHTYFNNVTMYYLNGATRDKLVMGVFPYGRAMSIEDRSKLGDPDA 300
QY 301 KGMSPPGFISGEGVLSYIELCOLFQKEEWHIOYDEYNNAPYGVNDKIWGYDDLASISC 360
DB 301 KGMSPPGFISGEGVLSYIELCOLFQKEEWHIOYDEYNNAPYGVNDKIWGYDDLASISC 360
QY 361 KLAFLKELGVSGVMVWVWLENDDFKHCQPKNPLLNKVNHNMGDEKNSFECILGPSTTTP 420
DB 361 KLAFLKELGVSGVMVWVWLENDDFKHCQPKNPLLNKVNHNMGDEKNSFECILGPSTTTP 420
QY 421 TPSTTTTHTSETPKYTYVDGHLIKCYKEGDIHPHTNIHKYLVCFVNGWVWHIMPCP 540
DB 421 TPSTTTTHTSETPKYTYVDGHLIKCYKEGDIHPHTNIHKYLVCFVNGWVWHIMPCP 540
QY 541 PGTINWQCEKLTICGE 555
DB 541 PGTINWQCEKLTICGE 555

RESULT 3

US-10-218-743-21
; Sequence 21, Application US/10218743
; Publication No. US20030096779A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/10/218,743
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/09/292,225
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: 60/098,909
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/085,295
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/098,565
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: 09/062,013
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 21
; LENGTH: 536
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-10-218-743-21

Query Match 97.0%; Score 3014; DB 14; Length 536;

Best Local Similarity 100.0%; Pred. No. 2e-213;
Matches 536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 320 ELCQLFQKEWHIOYDEYNNAPYGYNDKIWGYDDLASISCKLAFKELGVSVMVMSLE 379
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QY 380 NDDFKHGCGPKNPLKVNHNMGDEKNSFECILGPSITTTPTTPTTPTTPTTPTTPTTPT 439
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QY 440 TPT 499
Db 421 TPT 480

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RESULT 4
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; Sequence 35, Application US/10218743
; Publication No. US20030096779A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/10/218,743
; PRIOR FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/09/292,225
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: 60/098,909
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/085,295
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/098,565
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: 09/062,013
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 35
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-10-218-743-35

Query Match 81.8%; Score 2542; DB 14; Length 509;
Best Local Similarity 81.7%; Pred. No. 1e-178;

Matches 456; Conservative 24; Mismatches 26; Indels 52; Gaps 2;

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Db 1 MKTIYAILSIMACIGLMNASIIKRDNDYSKNPRIVCYVGTWSYHKVDYPTIEDIPFK 60

QY 61 CTHLMYGFADIKYKTIQVFPDYPQDDNHSWEKRGYERFNNLRKLNPELTWISLGGWY 120
Db 61 CTHLMYGFADIKYKTIQVFPDYPQDDNHSWEKRGYERFNNLRKLNPELTWISLGGWY 120

QY 121 EGSEKYSYDAAANTYRQOFIQSVLDFLOEYKFDGLDLDWEYPSGRGNPKIDKQNYLALV 180
Db 121 EGSEKYSYDAAANTYRQOFIQSVLDFLOEYKFDGLDLDWEYPSGRGNPKIDKQNYLALV 180

QY 181 RELKDAFEPHGYLLTAASPGKOKIDRAYDIKELNKLFDWMNVMTYDYGWENFYGHNA 240
Db 181 RELKDAFEPHGYLLTAASPGKOKIDRAYDIKELNKLFDWMNVMTYDYGWENFYGHNA 240

QY 241 PLYKRDETDDELHTYFNVNMTYDYGWENFYGHNAPLYKRPDETDELHTYFNVN 300
Db 241 PLYKRDETDDELHTYFNVNMTYDYGWENFYGHNAPLYKRPDETDELHTYFNVN 300

QY 301 KGMSPPGFISGEGVLSYIELCOLFOKEWHIOYDEYNNAPYGYNDKIWGYDDLASIS 360
Db 301 KGMSPPGFISGEGVLSYIELCOLFOKEWHIOYDEYNNAPYGYNDKIWGYDDLASIS 360

QY 361 KLAFLKELGVSVMVMSLENDDFKHCGRKPNLKNVHNMGDEKNSFECILGPSITTTPT 420
Db 361 KLAFLKELGVSVMVMSLENDDFKHCGRKPNLKNVHNMGDEKNSFECILGPSITTTPT 420

QY 421 TPT 480
Db 421 TPT 434

QY 481 TPT 537
Db 435 ---PTTDDTSSETPKVTYDGLIKCYKEGDIHPHTNIHKYLVCFFVNGWVHIM 491

QY 538 PCPPGTIWCQKLTICGE 555
Db 492 DCPKGRWHTATLKNICQE 509

RESULT 5
US-10-218-743-38
; Sequence 38, Application US/10218743
; Publication No. US20030096779A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/10/218,743
; PRIOR FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/09/292,225
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: 60/098,909
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/085,295
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/098,565
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: 09/062,013
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 38
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-10-218-743-38


```
Db 292 GAYTRQAGFWAYEICTFLRSGATEVM-----DASQEVFPYAYKANWLGVDNKSFSVKAQ 347
Qy 364 FLKELGVSVMWVLENDKFG-HCG-----PKNPLNKNVHNMINGDEKNSFECILGPSTT 418
Db 348 WLKNNFGGAMWALDUDFTGSCDQKFLPLSTLNA-----LGISTE 392
Qy 419 TPTPTTPTTPTTPTT 433
Db 393 GCTAPDVPSEPVTP 407

RESULT 10
US-10-161-547-4
; Sequence 4, Application US/10161547
; Publication No. US2003014216A1
; GENERAL INFORMATION:
; APPLICANT: Gray, Patrick W.
; TITLE OF INVENTION: CHITINASE CHITIN-BINDING FRAGMENTS
; FILE REFERENCE: 27866/35407
; CURRENT APPLICATION NUMBER: US/10/161,547
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US/09/267,574
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/039,198
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 466
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-161-547-4

Query Match 23.6%; Score 732; DB 14; Length 466;
Best Local Similarity 33.9%; Pred. No. 1.6e-45;
Matches 151; Conservative 85; Mismatches 151; Indels 58; Gaps 11;

Qy 34 RIVCYVGTWSVYHKVDP-YTIEDIDPKCTHLMYGFADIKYKTIQVDFPYQDDNHSW 92
Db 23 KLVCFYTNWAQYRQGEARFLPKDLPSCLTCHLIYAFAGMTHQLST-----TEW 71
Qy 93 EKRGYERFNNLRKNPELTMTISLGGWYEGSEKYSMDAANFYRQFIQSVDLFQYK 151
Db 72 NDELTLYQEFNGLKKNPKLTLLAIGWNFTQKFTDMVATANNRQTFVNSAIRFLKYS 131
Qy 152 FDGLDLDWEYVGSRLGNPKIDKQNYLALVRELKDAPEPHG-----YLITAAVSPGDK 204
Db 132 FDGLDLDWEYVGSQ-GSPAVDKERFTLVQLDLANAFQBEAQTSKGERLLLSAAVPAQTY 190
Qy 205 IDRAYDIKELNKLFDWNNVMTYDYGWENFYGHNAPLYKRPDETDELHTYFNNVNTMY 264
Db 191 VDAGYEVDKIAQNLDVFNLAAYDFHGSWEKVTGHNSPLYKQEBESGAAS-LNVDAVQ 249
Qy 265 YLNNGATRDKLVMGVPFYGRAMSIEDRSKLGDPKAGMSPPGFISGEEGVLSYIELCOL 324
Db 250 WLQKGTPEASKLILGMPTYGRSFTLASSSDTRVGAPATGSGTTPGFTKEGGLAYEVCWS 309
Qy 325 FQKEEHIQYDEYNAPYGVNDKIWGYDDLASISCKLAFELKELGVSVMWVLENDKFX 384
Db 310 KGATKQRIQ-DO--KVPIYFRDNQWGFDDVSEPKTKVSYLKQKGLGAMWALDLDFA 366
Qy 385 GHCQPKNPLNKNVHNMINGDEKNSFECILGPSTTPTTPTTPTTPTTPTTPTTPTT 444
Db 367 G-----FSCNQG-----RYPLIQTIRQELSULPLPSGT 394
Qy 445 PSPTPTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTT 469
Db 395 FELEV-PKPGQSEPEHGFSPGQDT 418

RESULT 11
US-10-004-219B-9
```

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; Sequence 9, Application US/10004219B
; Publication No. US20030087414A1
; GENERAL INFORMATION:
; APPLICANT: Macrozyme
; APPLICANT: Aerts, Johannes M.F.G.
; APPLICANT: Boot, Rolf G.
; TITLE OF INVENTION: A mammalian mucinase, its recombinant production, and
; TITLE OF INVENTION: its use in therapy or prophylaxis against diseases in
; TITLE OF INVENTION: which mucus is involved or infection diseases
; FILE REFERENCE: 2183-5136US
; CURRENT APPLICATION NUMBER: US/10/004,219B
; CURRENT FILING DATE: 2001-11-02
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 452
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1) (452)
; OTHER INFORMATION: /note="Mouse AMCase"
US-10-004-219B-9

Query Match 23.5%; Score 729.5; DB 14; Length 452;
Best Local Similarity 37.0%; Pred. No. 2.3e-45;
Matches 154; Conservative 69; Mismatches 144; Indels 49; Gaps 11;

Qy 35 IVCYVGTWSVYHK-VDPYTIEDIDPKCTHLMYGFADIKYKTIQVDFPYQDDNHSW- 92
Db 3 LICYFTNWAQYRPGIGSGFKPDDINPCLCTHLIYAFAGMNNETIT-----IENW 51
Qy 93 EKRGYERFNNLRKNPELTMTISLGGWYEGSEKYSMDAANFYRQFIQSVDLFQYK 152
Db 52 DVTLYKAFNDLKNRNSKLTLLAIGWNFTQKFTDMVATANNRQTFVNSAIRFLQYGF 111
Qy 153 DGLDLDWEYVGSRLGNPKIDKQNYLALVRELKDAPEPHG-----YLITAAVSPGDK 205
Db 112 DGLDLDWEYVGSQ-RSPPODKHLFTVLVKEMREAFQEAIESNRPRLMVTAAVAGISNI 170
Qy 206 DRAYDIKELNKLFDWNNVMTYDYGWENFYGHNAPLYKRPDETDELHTYFNNVNTMY 265
Db 171 QAGYIPELSKYLDFTHVTYDLHGSWEGYTGENSEPLYKYTETGS-NAYLNVYVWY 229
Qy 266 LNNGATRDKLVMGVPFYGRAMSIEDRSKLGDPKAGMSPPGFISGEEGVLSYIELCOL 325
Db 230 KNGGAPAEKLVIGFPEYGHFTFLRNPDSNGIGAPTSGDGPAGAYTRQAGFWAYEICTFL 289
Qy 326 QK---BEWHIQYDEYNAPYGVNDKIWGYDDLASISCKLAFELKELGVSVMWVLEND 382
Db 290 RSGATEVM---DASQEVFPYAYKANWLGVDNKSFSVKAQWLKQNNFGGAMWALDLD 345
Qy 383 FKG-HCG---PKNPLNKNVHNMINGDEKNSFECILGPSTTPTTPTTPTTPTTPTT 433
Db 346 FTGSCDQKFLPLSTLNA-----LGISTECTAPDVPSEPVTP 386

RESULT 12
US-10-161-547-14
; Sequence 14, Application US/10161547
; Publication No. US20030143216A1
; GENERAL INFORMATION:
; APPLICANT: Gray, Patrick W.
; APPLICANT: Tjoelker, Larry W.
; TITLE OF INVENTION: CHITINASE CHITIN-BINDING FRAGMENTS
; FILE REFERENCE: 27866/35407
; CURRENT APPLICATION NUMBER: US/10/161,547
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US/09/267,574
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/039,198
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-03-12
; NUMBER OF SEQ ID NOS: 39
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 373
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-161-547-14

Query Match      23.2%; Score 721.5; DB 14; Length 373;
Best Local Similarity 37.7%; Pred. No. 6.9e-45;
Matches 136; Conservative 83; Mismatches 117; Indels 25; Gaps 8;

QY 34 RIVCYGTWSVYHKVDP-VTIEDIDPFKTHLMYGFADKIDYKTIQVDFPYQDDNHNWSW 92
Db 2 KLVCYFTNWAQYRQGEARFLPKDLDPSLCTHLIYAFAGMTNHLST-----TEW 50

QY 93 -EKRGYERFNNLRKKNPELTMTISLGGWYEGSEKYSDMAANTYRQOFIQSVLDFLOEYK 151
Db 51 NDETLVQEFNGLKKNPKLKTLLAIGGNWFGTQKFTDMVATANNRQTFVNSAIRFLRKYS 110

QY 152 FDGLDLWVEYPGSRGLGNPKIDKQNYLALVRELKDAPEPHG-----YLLTAAVSPGKDK 204
Db 111 FDGLDLWVEYPGSQ--GSPAVDKERFTTLVQDLANAFQQAQTSQGERLLLSAAVPAQGTY 169

QY 205 IDRAYDIKELNKLFDMMNVTYDYGWENFYGHNAPLYKRPDDETLHTYFNNVNTMHY 264
Db 170 VDAGYEVDKIAQNLDVFNLMAYDFHGSWEKVTGHSNPLYKQESGAAS-LNVDAVQ 228

QY 265 YLNNGATRDKLVGMVPPFYGRAWSIEDRSKLGDPKAGMSPPGFTSGEEGLVSYIELCOL 324
Db 229 WLQGTTPASKLILGMPTYGSRFTLASSSDTRVGAPATSGTGPFTKEGGLAYEVCWSW 288

QY 325 FQKEWHIQDEYNNAPYGNDKIWKGYDDIASISCKLAFELKELGVSGVMVWSLENDDFK 384
Db 289 KGATKQRIQ-DQ--KVPYIFRDNQWVGDFDVSFKTKVSYLKQKGLGGAMVWALDDFA 345

QY 385 G 385
Db 346 G 346

RESULT 13
US-10-004-219B-14
; Sequence 14, Application US/10004219B
; Publication No. US20030087414A1
; GENERAL INFORMATION:
; APPLICANT: Macrozyme
; APPLICANT: Aerts, Johannes M.F.G.
; APPLICANT: Boot, Rolf G.
; TITLE OF INVENTION: A mammalian mucinase, its recombinant production, and
; TITLE OF INVENTION: its use in therapy or prophylaxis against diseases in
; TITLE OF INVENTION: which mucus is involved or infection diseases
; FILE REFERENCE: 2183-5136US
; CURRENT APPLICATION NUMBER: US/10/004,219B
; CURRENT FILING DATE: 2001-11-02
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)-(455)
; OTHER INFORMATION: /note="Human AMCase"
US-10-004-219B-14

Query Match      22.8%; Score 708.5; DB 14; Length 455;
Best Local Similarity 35.9%; Pred. No. 8.1e-44;
Matches 149; Conservative 75; Mismatches 154; Indels 37; Gaps 10;

QY 34 RIVCYGTWSVYHK-VDPYTIETIDPFKTHLMYGFADKIDYKTIQVDFPYQDDNHNWSW 92
Db 2 QLTCTVTNWAQYRQGLRFPMDNIDPCLCTHLIYAFAGRNNEIT-----IEW 50

QY 93 -EKRGYERFNNLRKKNPELTMTISLGGWYEGSEKYSDMAANTYRQOFIQSVLDFLOEYK 151
Db 51 NDVTLYQAFNGLKKNKNSQLTKLLAIGGNWFGTAPFTAMVSTPENRQTFITSVIKFLRQE 110

QY 152 FDGLDLWVEYPGSRGLGNPKIDKQNYLALVRELKDAPEPHG-----YLLTAAVSPGKDK 204
Db 111 FDGLDLWVEYPGSR--GSPQDQKHLFTVLVQEMREAFQEAQKQKPKPLMVTAAVAGISN 169

QY 205 IDRAYDIKELNKLFDMMNVTYDYGWENFYGHNAPLYKRPDDETLHTYFNNVNTMHY 264
Db 170 IQSGYEIPEQLSQYLDYTHWYDYLHGSWEYTGENSELYKYPTDGTGS-NAYLNDVYMWY 228

QY 265 YLNNGATRDKLVGMVPPFYGRAWSIEDRSKLGDPKAGMSPPGFTSGEEGLVSYIELCOL 324
Db 229 WIDNGAPAEKLVIGFPFYGHNFILSNFTGAPTSGAGPAGPYAKESGIWAYYEIC-T 287
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Db	117	FDGLDMDEYPTQGGSPD-DYDNFVILMAELNQAHAEGMLLTAASAGKATIDPAYNV	175
Qy	212	KEINKLFDWNNVTYDYHGGWENFYCHNAPLYKRP-DETDLHTYFNVNNTMEYYLNNGA	270
Db	176	PELSKSLDLINVTYDLRGAWDDYTHQSGLYAHPLDEGD--NAFLNVDFAISYWIEKGA	233
Qy	271	TRDKLVNGVFFYGRAWSIEDRSKLGDPAGKMSPPGFISGEEGVLSYIELCOLFOKEEW	330
Db	234	RGQIALGIFLYGRWCWTLASQQETGYYPAHQPGAAGDWTRSPGMLGYNEICYMRTTQDW	293
Qy	331	HIQYDEYYNAPGY---NDKIWVGDDLASISCKLAFKELGVSGVWWSLENDDFKGHC	387
Db	294	TVVDDPAMNEPYTYFPMMNINWCSYDHAASVAIKAEYAKSKGLAGTMWWSVETDDFRGLC	353
Qy	388	GPKNPLLNKVHNMINGDEKNSPECILGPSITTTTPTTTTPTTTTPTTTTPTTTTPTTSP	447
Db	354	H-----NRKYHLI-----KTMVEVFGGSIETP-----	376
Qy	448	TTTTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTT	507
Db	377	-----PPLPTTTTRDPNEFTTTTRAPP-----PG-----VHC	403
Qy	508	YKEGDIPHPTNIHKYLVCEF-VNGGWVHIMPCPPGTIWCQEKLTG	552
Db	404	TQGLNPDPLDCTHYILCSLNTSGYNEKEVECEGTLYNPQSYC	449

Search completed: March 22, 2004, 06:59:26
Job time : 113.679 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 22, 2004, 06:30:23 ; Search time 168.752 Seconds
(without alignments)
929.256 Million cell updates/sec

Title: US-09-662-293-18
Perfect score: 3107
Sequence: 1 MKTYAIIASIMACIGLMNAS.....IMPCPPGTTCQKLTICGE 555

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : A_Geneseq_29Jan04:*
1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001s:*
5: Geneseq2002s:*
6: Geneseq2003as:*
7: Geneseq2003bs:*
8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3107	100.0	555	AAV52523	House dus
2	3107	100.0	555	AAU96327	Der HMW-m
3	3107	100.0	555	AAU96328	Der HMW-m
4	3014	97.0	536	AAV52525	House dus
5	3014	97.0	536	AAU96329	Der HMW-m
6	2542	81.8	509	AAV52533	D. pteron
7	2542	81.8	509	AAU96337	Der HMW-m
8	2542	81.8	509	AAU96338	Der HMW-m
9	2475	79.7	490	AAV52535	D. pteron
10	2475	79.7	490	AAU96339	Der HMW-m
11	1008.5	32.5	525	ABP72636	Anopheles
12	854.5	27.5	498	ABP72635	Drosophila
13	838.5	27.0	554	AAW01824	Manduca s
14	838.5	27.0	554	AAW01824	Manduca s
15	838.5	27.0	554	AAW01824	Manduca s
16	837.5	27.0	467	ABP72634	Prawn chi
17	837.5	27.0	565	ABP72625	Bombyx mo
18	837.5	27.0	595	ABP71737	Drosophila
19	832	26.8	460	ABP72636	Drosophila
20	815.5	26.2	583	AAE28197	Flea chit
21	812.5	26.2	635	AAE28203	Flea chit
22	811.5	26.1	559	AAE28203	Flea chit
23	810	26.1	574	ABP72635	Aedes aeg
24	802	25.8	483	ABP72633	Chelonus
25	787	25.3	553	ABP72626	Hyphantria

26	738	23.8	466	2	AAW08584	Human 50
27	738	23.8	466	2	AAW40259	Human chi
28	738	23.8	466	2	AAW42425	MO-218 cl
29	738	23.8	466	4	AAE00432	Human chi
30	738	23.8	466	5	AAE25903	Human chi
31	738	23.8	466	5	ABB76291	Human chi
32	737.5	23.7	520	6	ABU09914	Partial m
33	736.5	23.7	473	7	ABR55543	Amino aci
34	735.5	23.7	459	7	ADC24231	Human NOV
35	734.5	23.6	473	7	ADC51464	Chitotria
36	732.5	23.6	387	2	AAW08585	Human 39
37	732	23.6	447	7	ADC24237	Human NOV
38	732	23.6	466	2	AAW40260	Human chi
39	732	23.6	466	2	AAW42426	MO-13B cl
40	732	23.6	466	4	AAE00433	Human chi
41	732	23.6	466	5	AAE25904	Human chi
42	732	23.6	466	5	ABB76292	Human chi
43	731	23.5	466	2	AAW31498	Human chi
44	729.5	23.5	452	7	ABR55544	Amino aci
45	723	23.3	466	6	ABP72621	Human chi

ALIGNMENTS

RESULT 1
AAV52523
ID AAV52523 standard; protein; 555 AA.
XX AC AAV52523;
XX AC AAV52523;
DT 22-FEB-2000 (first entry)
XX DE House dust mite (D. farinae) mite allergen protein (map) PDerf98-555.
XX KW Mite allergen protein; map; high molecular weight; HMW-map; allergy;
XX KW house dust mite; IGE; immunoglobulin E; allergen; mapA; mapB;
XX KW hypersensitivity reaction; therapy; treatment; diagnosis; human; feline;
XX KW canine; veterinary; antibody; vaccine; immunisation.
XX OS Dermatophagoides farinae.
XX FH Key Location/Qualifiers
FT Peptide 1..19
FT Protein /note= "Signal peptide"
FT Protein 20..555
FT Protein /note= "Mature Pderf98-555"

XX FN WO9954349-A2.
XX PD 28-OCT-1999.
XX PF 16-APR-1999; 99WO-US008524.
XX PR 17-APR-1998; 98US-00062013.
XX PR 13-MAY-1998; 98US-0085295P.
XX PR 02-SEP-1998; 98US-0098909P.
XX PA (HESK-) HESKA CORP.
XX PI McCall CA, Hunter SW, Weber ER;
XX PI WPI; 2000-052700/04.
XX DR N-PSDB; AAZ38575, AAZ38576, AAZ38577, AAZ38578.
XX DR Novel high molecular weight Dermatophagoides nucleic acid polypeptides used to modify an animals' hypersensitivity to mite allergens.
XX PT Claim 3; Page 111-113; 154pp; English.
XX PS This sequence represents Dermatophagoides farinae mite allergen protein (map) PDerf98-555. Pderf98-555 has a molecular weight of 98 kD, comprising 555 amino acids, and is a component of the Dermatophagoides

CC farinae high molecular weight mite allergen protein (HMW-map)
CC composition. The HMW-map composition was isolated from a D. farinae
CC homogenate by gel filtration, with each fraction being analysed for the
CC presence of proteins that bound to IgE present in mite-allergic dog
CC antisera. Mite allergenic proteins and peptides, and nucleic acids
CC encoding them, may be used in therapeutic compositions to modify an
CC animal's hypersensitivity reaction to mite allergens. Animals that may be
CC treated include mammals and birds, especially felines, canines, equines,
CC humans, other pets, and work or domestic animals. The proteins or
CC fragments may also be used to diagnose allergies via a skin test. The
CC proteins and peptides can also be used to raise antibodies, which have a
CC variety of potential uses. For example, they can be used as vaccines to
CC passively immunise animals against dust mite hypersensitivity, as
CC positive controls in test kits and as tools to recover desired dust mite
CC allergens from a mixture of proteins
XX
SQ Sequence 555 AA;

Query Match 100.0%; Score 3107; DB 3; Length 555;
Best Local Similarity 100.0%; Pred. No. 1.8e-217;
Matches 555; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKTIVAILSIMACIGLMNASIKRDHNDYSKNPMRIVCVGTWSVYHKVDPTTIEDIDPFK 60
DB 1 MKTIVAILSIMACIGLMNASIKRDHNDYSKNPMRIVCVGTWSVYHKVDPTTIEDIDPFK 60
QY 61 CTHLMYGFADIEYKTYIQVDFPYQDDHNSWEKRGYERFNNLRKNPELTMTISLGWY 120
DB 61 CTHLMYGFADIEYKTYIQVDFPYQDDHNSWEKRGYERFNNLRKNPELTMTISLGWY 120
QY 121 EGSEKYSDMAANPTVYRQOFTQSVLDLQYKFDGLDWEYPSGLGNPKIDQNYLALV 180
DB 121 EGSEKYSDMAANPTVYRQOFTQSVLDLQYKFDGLDWEYPSGLGNPKIDQNYLALV 180
QY 181 RELKDAFEPHYLLTAASVPGKDKIDRAYDIKELNKLFDWMNVMTYDYGHWENFYGHNA 240
DB 181 RELKDAFEPHYLLTAASVPGKDKIDRAYDIKELNKLFDWMNVMTYDYGHWENFYGHNA 240
QY 241 PLYKRPDETDELHTYFNVNNTMYHLLNNGATRDKLVMGVFFYGRANSIEDRSKLGDP 300
DB 241 PLYKRPDETDELHTYFNVNNTMYHLLNNGATRDKLVMGVFFYGRANSIEDRSKLGDP 300
QY 301 KGMSPPGFISGEEGVLSIELCQLFQKEWHIQVDEYNNAPYGYNDKIWGYDDLASISC 360
DB 301 KGMSPPGFISGEEGVLSIELCQLFQKEWHIQVDEYNNAPYGYNDKIWGYDDLASISC 360
QY 361 KLAFLKELGVSGVMVWSLENDDFKHCPCPKNPLNKHVNMINGDEKNSFECILGPSTTP 420
DB 361 KLAFLKELGVSGVMVWSLENDDFKHCPCPKNPLNKHVNMINGDEKNSFECILGPSTTP 420
QY 421 TPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTT 480
DB 421 TPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTT 480
QY 481 TPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTT 540
DB 481 TPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTT 540
QY 541 PGTIWCQKLTICGE 555
DB 541 PGTIWCQKLTICGE 555

RESULT 2

AAU96327
ID AAU96327 standard; protein; 555 AA.

XX AC AAU96327;

XX DT 15-JUL-2002 (first entry)

XX DE Der HMW-map polypeptide #14.

XX

KW Der HMW-map; American house dust mite; antiallergic; mite; IgE;
KW mite allergenic protein; immunoglobulin E; hypersensitivity;
KW immunocomplex formation.
XX
OS Dermatophagoides farinae.
PN WO200222807-A2.
XX
PD 21-MAR-2002.
PF 14-SEP-2001; 2001WO-US028730.
XX
PR 14-SEP-2000; 2000US-00662293.
XX
PA (HESK-) HESKA CORP.
XX
PI McCall CA, Hunter SW, Weber ER;
XX
DR WPI; 2002-351888/38.
DR N-PSDB; ABK69571.
XX
PT New mite allergenic protein isolated from Dermatophagoides, designated
PT Der HMW-map protein, useful as a vaccine for treating mite allergy.
XX
PS Claim 12; Page 114-116; 161pp; English.

CC The invention relates to an isolated mite allergenic protein of
CC Dermatophagoides, designated Der HMW-map protein, and its related nucleic
CC acid. The Der HMW-map protein is useful for eliciting an immune response
CC against Der HMW-map protein. The protein or a reagent comprising a non-
CC proteinaceous epitope is useful for identifying an animal (e.g., dog,
CC cat) susceptible to or having an allergic response to a mite. A
CC therapeutic composition is useful for desensitising a host animal to an
CC allergic response to a mite. The DNA and protein can be used in the
CC detection of anti-Der HMW-map antibodies in animal fluids, and inhibition
CC of immunoglobulin (Ig)E or Der HMW-map protein activity associated with a
CC disease. Antibodies that bind to Der HMW-map are useful for inhibiting
CC binding of proteins to IgE, to prevent immunocomplex formation, thus
CC reducing hypersensitivity responses to mite allergens, and as vaccines
CC against mite allergen hypersensitivity. Sequences AAU96314-AAU96342
CC represent Der HMW-map polypeptides of the invention

XX Sequence 555 AA;

Query Match 100.0%; Score 3107; DB 5; Length 555;
Best Local Similarity 100.0%; Pred. No. 1.8e-217;
Matches 555; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKTIVAILSIMACIGLMNASIKRDHNDYSKNPMRIVCVGTWSVYHKVDPTTIEDIDPFK 60
DB 1 MKTIVAILSIMACIGLMNASIKRDHNDYSKNPMRIVCVGTWSVYHKVDPTTIEDIDPFK 60
QY 61 CTHLMYGFADIEYKTYIQVDFPYQDDHNSWEKRGYERFNNLRKNPELTMTISLGWY 120
DB 61 CTHLMYGFADIEYKTYIQVDFPYQDDHNSWEKRGYERFNNLRKNPELTMTISLGWY 120
QY 121 EGSEKYSDMAANPTVYRQOFTQSVLDLQYKFDGLDWEYPSGLGNPKIDQNYLALV 180
DB 121 EGSEKYSDMAANPTVYRQOFTQSVLDLQYKFDGLDWEYPSGLGNPKIDQNYLALV 180
QY 181 RELKDAFEPHYLLTAASVPGKDKIDRAYDIKELNKLFDWMNVMTYDYGHWENFYGHNA 240
DB 181 RELKDAFEPHYLLTAASVPGKDKIDRAYDIKELNKLFDWMNVMTYDYGHWENFYGHNA 240
QY 241 PLYKRPDETDELHTYFNVNNTMYHLLNNGATRDKLVMGVFFYGRANSIEDRSKLGDP 300
DB 241 PLYKRPDETDELHTYFNVNNTMYHLLNNGATRDKLVMGVFFYGRANSIEDRSKLGDP 300
QY 301 KGMSPPGFISGEEGVLSIELCQLFQKEWHIQVDEYNNAPYGYNDKIWGYDDLASISC 360
DB 301 KGMSPPGFISGEEGVLSIELCQLFQKEWHIQVDEYNNAPYGYNDKIWGYDDLASISC 360
QY 361 KLAFLKELGVSGVMVWSLENDDFKHCPCPKNPLNKHVNMINGDEKNSFECILGPSTTP 420

DR WPI; 2000-052700/04.
XX N-PSDB; AA238579, AA238580.
PT Novel high molecular weight Dermatophagoides nucleic acid polypeptides
PT used to modify an animals' hypersensitivity to mite allergens.
XX
XX Claim 3; Page 125-127; 154pp; English.
XX
XX This sequence represents Dermatophagoides farinae mite allergen protein
CC (map) pDerf98-536, the mature form of pDerf98-555 (AAV52523). pDerf98-536
CC has a molecular weight of 98 kD, comprising 536 amino acids, and is a
CC component of the Dermatophagoides farinae high molecular weight mite
CC allergen protein (HWM-map) composition. The HWM-map composition was
CC isolated from a D. farinae homogenate by gel filtration, with each
CC fraction being analysed for the presence of proteins that bound to IgE
CC present in mite-allergic dog antiserum. Mite allergenic proteins and
CC peptides, and nucleic acids encoding them, may be used in therapeutic
CC compositions to modify an animal's hypersensitivity reaction to mite
CC allergens. Animals that may be treated include mammals and birds,
CC especially felines, canines, equines, humans, other pets, and work or
CC domestic animals. The proteins or fragments may also be used to diagnose
CC allergies via a skin test. The proteins and peptides can also be used to
CC raise antibodies, which have a variety of potential uses. For example,
CC they can be used as vaccines to passively immunise animals against dust
CC mite hypersensitivity, as positive controls in test kits and as tools to
CC recover desired dust mite allergens from a mixture of proteins
XX
XX Sequence 536 AA;
SQ

Query Match 97.0%; Score 3014; DB 3; Length 536;
Best Local Similarity 100.0%; Pred. No. 1e-210;
Matches 536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 SIKRDNDYKSNPMRIVCYVGTWSVYHKVDPTYTIEDIDPFKCHLMYGFAKIDYKTYIQ 79
DB 1 SIKRDNDYKSNPMRIVCYVGTWSVYHKVDPTYTIEDIDPFKCHLMYGFAKIDYKTYIQ 60
QY 80 VFDPYQDDNHNSEKRGYERFNNLRKLNPELTTMISLGWYEGSEKYSDMAANPTYRQOF 139
DB 61 VFDPYQDDNHNSEKRGYERFNNLRKLNPELTTMISLGWYEGSEKYSDMAANPTYRQOF 120
QY 140 IQSVLDFLOEYKFDGLDWEYFGSLGNPKIDKQNYLALVRELKDAFPHGYLLTAAYS 199
DB 121 IQSVLDFLOEYKFDGLDWEYFGSLGNPKIDKQNYLALVRELKDAFPHGYLLTAAYS 180
QY 200 PGKDKIDRAYDIKELNKLFDWMNVMTYDYGHWENFYGHNAPLYKRPDETDELHTYFNVN 259
DB 181 PGKDKIDRAYDIKELNKLFDWMNVMTYDYGHWENFYGHNAPLYKRPDETDELHTYFNVN 240
QY 260 YTHYLYNNGATRDKLVGMVGFYFGRAWSTEDRSKLKLGDPKAGMSPPGFISGEGVLSYI 319
DB 241 YTHYLYNNGATRDKLVGMVGFYFGRAWSTEDRSKLKLGDPKAGMSPPGFISGEGVLSYI 300
QY 320 ELCOLFKQKEBWHIYDEYNNAPYGYNDKIWGVYDDLASISCKLAFELKELGVSGVMVWSLE 379
DB 301 ELCOLFKQKEBWHIYDEYNNAPYGYNDKIWGVYDDLASISCKLAFELKELGVSGVMVWSLE 360
QY 380 NDFKKGCHGCPKNLLKNVHNKNGDEKNSPECILGPSTTPTPTPTPTPTPTPTPTPTPTPT 439
DB 361 NDFKKGCHGCPKNLLKNVHNKNGDEKNSPECILGPSTTPTPTPTPTPTPTPTPTPTPTPT 420
QY 440 TPT 499
DB 421 TPT 480
QY 500 VDGHLLKCYKEGDIPIHPTNTHKYLVECFVNGGWHVHIMPCPGTINWCQKLCIGE 555
DB 481 VDGHLLKCYKEGDIPIHPTNTHKYLVECFVNGGWHVHIMPCPGTINWCQKLCIGE 536

RESULT 5
AAU96329
ID AAU96329 standard; protein; 536 AA.

XX AAU96329;
XX 15-JUL-2002 (first entry)
XX
XX Der HWM-map polypeptide #16.
XX
XX Der HWM-map; American house dust mite; antiallergic; mite; IgE;
KW mite allergenic protein; immunoglobulin E; hypersensitivity;
KW immunocomplex formation.
XX
XX Dermatophagoides farinae.
XX WO200222807-A2.
XX 21-MAR-2002.
XX 14-SEP-2001; 2001WO-US028730.
XX 14-SEP-2000; 2000US-00662293.
XX (HESK-) HESKA CORP.
XX McCall CA, Hunter SW, Weber ER;
PI WPI; 2002-351888/38.
XX N-PSDB; ABK69575.
XX
XX New mite allergenic protein isolated from Dermatophagoides, designated
PT Der HWM-map protein, useful as a vaccine for treating mite allergy.
XX
XX Claim 12; Page 125-127; 161pp; English.
XX
XX The invention relates to an isolated mite allergenic protein of
CC Dermatophagoides, designated Der HWM-map protein, and its related nucleic
CC acid. The Der HWM-map protein is useful for eliciting an immune response
CC against Der HWM-map protein. The protein or a reagent comprising a non-
CC proteinaceous epitope is useful for identifying an animal (e.g., dog,
CC cat) susceptible to or having an allergic response to a mite. A
CC therapeutic composition is useful for desensitising a host animal to an
CC allergic response to a mite. The DNA and protein can be used in the
CC detection of anti-Der HWM-map antibodies in animal fluids, and inhibition
CC of immunoglobulin (Ig)E or Der HWM-map protein activity associated with a
CC disease. Antibodies that bind to Der HWM-map are useful for inhibiting
CC binding of proteins to IgE, to prevent immunocomplex formation, thus
CC reducing hypersensitivity responses to mite allergens, and as vaccines
CC against mite allergen hypersensitivity. Sequences AAU96314-AAU96342
CC represent Der HWM-map polypeptides of the invention
XX
XX Sequence 536 AA;
SQ

Query Match 97.0%; Score 3014; DB 5; Length 536;
Best Local Similarity 100.0%; Pred. No. 1e-210;
Matches 536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 SIKRDNDYKSNPMRIVCYVGTWSVYHKVDPTYTIEDIDPFKCHLMYGFAKIDYKTYIQ 79
DB 1 SIKRDNDYKSNPMRIVCYVGTWSVYHKVDPTYTIEDIDPFKCHLMYGFAKIDYKTYIQ 60
QY 80 VFDPYQDDNHNSEKRGYERFNNLRKLNPELTTMISLGWYEGSEKYSDMAANPTYRQOF 139
DB 61 VFDPYQDDNHNSEKRGYERFNNLRKLNPELTTMISLGWYEGSEKYSDMAANPTYRQOF 120
QY 140 IQSVLDFLOEYKFDGLDWEYFGSLGNPKIDKQNYLALVRELKDAFPHGYLLTAAYS 199
DB 121 IQSVLDFLOEYKFDGLDWEYFGSLGNPKIDKQNYLALVRELKDAFPHGYLLTAAYS 180
QY 200 PGKDKIDRAYDIKELNKLFDWMNVMTYDYGHWENFYGHNAPLYKRPDETDELHTYFNVN 259
DB 181 PGKDKIDRAYDIKELNKLFDWMNVMTYDYGHWENFYGHNAPLYKRPDETDELHTYFNVN 240
QY 260 YTHYLYNNGATRDKLVGMVGFYFGRAWSTEDRSKLKLGDPKAGMSPPGFISGEGVLSYI 319

Db 241 YTMHYLNGATRDKLWGVPPYGRANSIEDRSKULGDPAGKMPGFIISGEGVLSYI 300
QY 320 ELCCQLFQKEEWHIQDEYNNAPYNDKILWGYDDLASISCKLAFKELGSGVNVWSLE 379
Db 301 ELCCQLFQKEEWHIQDEYNNAPYNDKILWGYDDLASISCKLAFKELGSGVNVWSLE 360
QY 380 NDDFKGHCQKPNLKNVNMINGDEKNSFECILGSPSTTPPTTPPTTPPTTPPT 439
Db 361 NDDFKGHCQKPNLKNVNMINGDEKNSFECILGSPSTTPPTTPPTTPPTTPPT 420
QY 440 TPTTTPSPPTTPPTTPPTTPPTTPPTTPPTTPPTTPPTTPPTTPPTTPPTTP 499
Db 421 TPTTTPSPPTTPPTTPPTTPPTTPPTTPPTTPPTTPPTTPPTTPPTTPPT 480
QY 500 VDGHLIKCYKEGDIHPHTNIHKYLVCFFVNGGWWHIMPCPGTIWCQEKLTICGE 555
Db 481 VDGHLIKCYKEGDIHPHTNIHKYLVCFFVNGGWWHIMPCPGTIWCQEKLTICGE 536

RESULT 6
AAV52533
ID AAV52533 standard; protein; 509 AA.
XX AC
XX AAV52533;
XX DT 06-AUG-2003 (revised)
XX DT 22-FEB-2000 (first entry)
XX DE D. pteronyssius 98 kD mite allergen protein (map) PDerp98-509.
XX KW Mite allergen protein; map; high molecular weight; HMW-map; allergy;
XX KW house dust mite; IgE; immunoglobulin E; allergen; mapB;
XX KW hypersensitivity reaction; therapy; treatment; diagnosis; human; feline;
XX KW canine; veterinary; antibody; vaccine; immunisation.
XX OS Dermatophagoides pteronyssinus.
XX FH Key Location/Qualifiers
FT Peptide 1..19 /note= "Signal peptide"
FT FT 20..509
FT Protein /note= "Mature PDerp98-509"
XX WO9954349-A2.
XX 28-OCT-1999.
XX 16-APR-1999; 99WO-US008524.
XX 17-APR-1998; 98US-00062013.
XX 13-MAY-1998; 98US-0085295P.
XX 02-SEP-1998; 98US-0098909P.
XX (HESK-) HESKA CORP.
XX Mccall CA, Hunter SW, Weber ER;
XX WPI; 2000-052700/04.
XX N-PSDB; AAZ38585, AAZ38586, AAZ38587, AAZ38588.
XX Novel high molecular weight Dermatophagoides nucleic acid polypeptides
XX used to modify an animals' hypersensitivity to mite allergens.
XX Claim 3; Page 134-136; 154pp; English.

This sequence represents Dermatophagoides pteronyssius mite allergen protein (map) PDerp98-509. PDerp98-509 has a molecular weight of 98 kD, comprising 509 amino acids, and has a high degree of homology with the D. farinae 98 kD allergen, mapB (AAV52523). Nucleic acid molecules encoding PDerp98-509 were isolated from a D. pteronyssius cDNA library by hybridisation with a probe encoding the D. farinae high molecular weight map (HMW-map) composition. Mite allergenic proteins and peptides, and nucleic acids encoding them, may be used in therapeutic compositions to

CC modify an animal's hypersensitivity reaction to mite allergens. Animals
CC that may be treated include mammals and birds, especially felines,
CC canines, equines, humans, other pets, and work or domestic animals. The
CC proteins or fragments may also be used to diagnose allergies via a skin
CC test. The proteins and peptides can also be used to raise antibodies,
CC which have a variety of potential uses. For example, they can be used as
CC vaccines to passively immunise animals against dust mite
CC hypersensitivity, as positive controls in test kits and as tools to
CC recover desired dust mite allergens from a mixture of proteins. (Updated
CC on 06-AUG-2003 to correct OS field.)
XX Sequence 509 AA;
SQ

Query Match 81.8%; Score 2542; DB 3; Length 509;
Best Local Similarity 81.7%; Pred. No. 2e-176;
Matches 456; Conservative 24; Mismatches 26; Indels 52; Gaps 2;
QY 1 MKTVAIISLMACIGLNNASIKRDNDYSKNPMRIVCVGTWSVYHKVDPYTIEDIDPFK 60
Db 1 MKTTFALFCIWACIGLNNAAKRDNNYSKNPMRIVCVGTWSVYHKVDPYTIEDIDPFK 60
QY 61 CTHLMYGFPAKIDYKTIQVDPDYQDDNHNHSEKRGYERFNNLRLKNPELTMTISLGWY 120
Db 61 CTHLMYGFPAKIDYKTIQVDPDYQDDNHNHSEKRGYERFNNLRLKNPELTMTISLGWY 120
QY 121 EGSEKYSDMAANPTYRQFQSVLDLDFLOEYKFDGLDWEYPGSRLGNPKIDKQNYLTV 180
Db 121 EGSEKYSDMAANPTYRQFQSVLDLDFLOEYKFDGLDWEYPGSRLGNPKIDKQNYLTV 180
QY 181 RELKDAFPHGYLLTAAVSPGKIDRAYDIKELNKLFDANNVMTYDYGHWENFYGHNA 240
Db 181 RELKEAFPFPGYLLTAAVSPGKIDVAYELKELNQLFDANNVMTYDYGHWENFYGHNA 240
QY 241 PLYKRPDETDLHTYFNVNYTHYLLANGATRDKLWGVPPYGRANSIEDRSKVLGDP 300
Db 241 PLYKRPDETDLHTYFNVNYTHYLLANGATRDKLWGVPPYGRANSIEDRSKVLGDP 300
QY 301 KGMSPPGTISGEGVLSYIELCOLFQKEEWHIQDEYNNAPYGYNDKILWGYDDLASISC 360
Db 301 KGMSPPGTISGEGVLSYIELCOLFQKEEWHIQDEYNNAPYGYNDKILWGYDDLASISC 360
QY 361 KLAFKELGSGVNVWSLENDDFKHCQKPNLKNVNMINGDEKNSFECILGSPSTTP 420
Db 361 KLAFKELGSGVNVWSLENDDFKHCQKPNLKNVNMINGDEKNSFECILGSPSTTP 420
QY 421 TPTTTPPTTPPTTPPTTPPTTPPTTPPTTPPTTPPTTPPTTPPTTPPTTPPT 480
Db 421 TPTTTPPTTPPTTPPTTPPTTPPTTPPTTPPTTPPTTPPTTPPTTPPTTPPT 434
QY 481 TPTTTPPTTPPTTPPTTPPTTPPTTPPTTPPTTPPTTPPTTPPTTPPTTPPT 537
Db 435 ---PTTDTSTSETPKYTYIDGHLIKCYKQGYLPHPTDVHKYLVCYIATPNGGWWHIM 491

RESULT 7
AAU96337
ID AAU96337 standard; protein; 509 AA.
XX AC
XX AAU96337;
XX 15-JUL-2002 (first entry)
XX Der HMW-map polypeptide #24.
XX Der HMW-map; American house dust mite; antiallergic; mite; IgE;
XX mite allergenic protein; immunoglobulin E; hypersensitivity;
XX immunocomplex formation.
XX Dermatophagoides farinae.
OS

[illegible]

QY 61 CTHLMYGFADIKYKTIQVDFPYQDDNHNSEKGYERFNNLRKNPELTMTMISLGGWY 120
DB 61 CTHLMYGFADIKYKTIQVDFPYQDDNHNSEKGYERFNNLRKNPELTMTMISLGGWY 120
QY 121 EGSEKSDMAANTYRQOFTOSVLDLQYKFGDLWDWEYFPGSRGNPKIDKQNTLALV 180
DB 121 EGSEKSDMAANTYRQOFTOSVLDLQYKFGDLWDWEYFPGSRGNPKIDKQNTLALV 180
QY 181 RELKDAPEPHGYLLTAASVPGKDKIDRAYDIKELNKLFDMMNVTYDYGWENFYGHNA 240
DB 181 RELKDAPEPHGYLLTAASVPGKDKIDRAYDIKELNKLFDMMNVTYDYGWENFYGHNA 240
QY 241 PLYKRPDETDELHTYFNVTMTHYLLNNGATRDKLVMGVFFYGRAWSIEDRSKLGDPDA 300
DB 241 PLYKRPDETDELHTYFNVTMTHYLLNNGATRDKLVMGVFFYGRAWSIEDRSKLGDPDA 300
QY 301 KGMSPGFGISGEGVLSYIELCOLFOKEWHIOYDEYNAPYNDKIWGVYDDLASISC 360
DB 301 KGMSPGFGISGEGVLSYIELCOLFOKEWHIOYDEYNAPYNDKIWGVYDDLASISC 360
QY 361 KLAFLKELGVGMVWSLENDPKHGCGPKNPILLNKVHNMINGDEKNSYECILGPSTTTP 420
DB 361 KLAFLKELGVGMVWSLENDPKHGCGPKNPILLNKVHNMINGDEKNSYECILGPSTTTP 420
QY 421 TPPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTT 480
DB 421 TPPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTT 480
QY 481 TPSTTTEHTSETPKTYTYVDGHLIKYKREGDIPHTNTHKYLVCBFV---NGGWWVHIM 537
DB 435 ---PTTDTSTSETPKTYTYVDGHLIKYKQGYLPHPTDVHKYLVCYIATPNGGWWVHIM 491
QY 538 PCPPGTIWCQKLTICGE 555
DB 492 DCPKGRWHTATLNCIQE 509
RESULT 9
AAV52535
ID RAY52535 standard; protein; 490 AA.
AC AAV52535;
XX
XX
DT 06-AUG-2003 (revised)
DT 22-FEB-2000 (first entry)
XX
DE D. pteronyssius 98 kD mite allergen protein (map) Pderp98-490.
XX Mite allergen protein; map; high molecular weight; HMW-map; allergy;
XW house dust mite; IgE; immunoglobulin E; allergen; mapB;
XW hypersensitivity reaction; therapy; treatment; diagnosis; human; feline;
XW canine; veterinary; antibody; vaccine; immunisation.
OS Dermatophagoides pteronyssinus.
XX
FH Key Location/Qualifiers
FT Modified-site 115..117
FT /note= "Asn is N-glycosylated"
FT Modified-site 240..242
FT /note= "Asn is N-glycosylated"
XX
PN MO9954349-A2.
XX
XX
PD 28-OCT-1999.
XX
PF 16-APR-1999; 99WO-US008524.
XX
PR 17-APR-1998; 98US-00062013.
PR 13-MAY-1998; 98US-0085295P.
PR 02-SEP-1998; 98US-0098909P.
XX
XX (HESK-) HESKA CORP.
XX

PI McCall CA, Hunter SW, Weber ER;
XX WPI: 2000-052700/04.
DR N-PSDB; AAZ38589, AAZ38590.
XX
PT Novel high molecular weight Dermatophagoides nucleic acid polypeptides
FT used to modify an animals' hypersensitivity to mite allergens.
XX
PS Claim 3; Page 147-149; 154pp; English.
XX
CC This sequence represents Dermatophagoides pteronyssius mite allergen
CC protein (map) Pderp98-490, the mature form of pDerp98-509. Pderp98-490
CC has a molecular weight of 98 kD, comprising 490 amino acids, and has a
CC high degree of homology with the D. farinae mature 98 kD allergen, mapB
CC (AAV52535). Nucleic acid molecules encoding Pderp98-490 were isolated
CC from a D. pteronyssius cDNA library by hybridisation with a probe
CC encoding the D. farinae high molecular weight map (HMW-map) composition.
CC Mite allergenic proteins and peptides, and nucleic acids encoding them,
CC may be used in therapeutic compositions to modify an animal's
CC hypersensitivity reaction to mite allergens. Animals that may be treated
CC include mammals and birds, especially felines, canines, equines, humans,
CC other pets, and work or domestic animals. The proteins or fragments may
CC also be used to diagnose allergies via a skin test. The proteins and
CC peptides can also be used to raise antibodies, which have a variety of
CC potential uses. For example, they can be used as vaccines to passively
CC immunise animals against dust mite hypersensitivity, as positive controls
CC in test kits and as tools to recover desired dust mite allergens from a
CC mixture of proteins. (Updated on 06-AUG-2003 to correct OS field.)
XX
SQ Sequence 490 AA;
Query Match 79.7%; Score 2475; DB 3; Length 490;
Best Local Similarity 82.5%; Pred. No. 1.5e-171;
Matches 443; Conservative 21; Mismatches 21; Indels 52; Gaps 2;
QY 22 KRDNHNSKPMRIVCVYGTWSVYHKVDPTIEDIPKCTHLMYGFADIKYKTIQV 81
DB 3 KRDNHNSKPMRIVCVYGTWSVYHKVDPTIEDIPKCTHLMYGFADIKYKTIQV 62
QY 82 DPYQDDNHNSEKGYERFNNLRKNPELTMTMISLGGWYEGSEKYSYDMMANPTVROQFIQ 141
DB 63 DPFQDDNHNSEKGYERFNNLRKNPELTMTMISLGGWYEGSEKYSYDMMANPTVROQFVQ 122
QY 142 SVLDLQYKFGDLWDWEYFPGSRGNPKIDKQNTLALVRELKDAPEPHGYLLTAASVPG 201
DB 123 SVLDLQYKFGDLWDWEYFPGSRGNPKIDKQNTLALVRELKDAPEPHGYLLTAASVPG 182
QY 202 KDKIDRAYDIKELNKLFDMMNVTYDYGWENFYGHNAPLYKRPDETDELHTYFNVT 261
DB 183 KDKIDVAYELKELNQLFDMMNVTYDYGWENFYGHNAPLYKRPDETDELHTYFNVT 242
QY 262 MHYLLNNGATRDKLVMGVFFYGRAWSIEDRSKLGDPKGMSPGFGISGEGVLSYIEL 321
DB 243 MHYLLNNGATRDKLVMGVFFYGRAWSIEDRSKLGDPKGMSPGFGISGEGVLSYIEL 302
QY 322 COLFOKEWHIOYDEYNAPYNDKIWGVYDDLASISCKLAFKELGVSGVWWSLEND 381
DB 303 COLFOKEWHIOYDEYNAPYNDKIWGVYDDLASISCKLAFKELGVSGVWWSLEND 362
QY 382 DFKHGCGPKNPILLNKVHNMINGDEKNSYECILGPSTTPTTPTTPTTPTTPTTPTTPTT 441
DB 363 DFKHGCGPKNPILLNKVHNMINGDEKNSYECILGPSTTPTTPTTPTTPTTPTTPTTPTT 415
QY 442 TPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTT 501
DB 416 -----PTTDTSTSETPKTYTYVD 433
QY 502 GHLIKYKREGDIPHTNTHKYLVCBFV---NGGWWVHIMPCPGTINCOEKLTCIGE 555
DB 434 GHLIKYKQGYLPHPTDVHKYLVCYIATPNGGWWVHIMDCPKGRWHTATLNCIQE 490
RESULT 10

AAU96339	standard; protein; 490 AA.	
ID	AAU96339	262 MHYLLNGATRDKLVGVPPFYGRAWSIEDRSKVLKLGDPAGKMGPPPGFISGEGVLSYIEL 321
XX		
AC	AAU96339;	243 MHYLLNGATRDKLVGVPPFYGRAWSIEDRSKVLKLGDPAGKMGPPPGFISGEGVLSYIEL 302
XX		
DT	15-JUL-2002 (first entry)	322 COLFQKEWHIOYDEYVNPAGYNDKLVGVDDIASISCKLAFKELGVGVWVWSLEND 381
XX		
DE	Der HMW-map polypeptide #26.	303 COLFQKEWHIOYDEYVNPAGYNDKLVGVDDIASISCKLAFKELGVGVWVWSLEND 362
XX		
KW	Der HMW-map; American house dust mite; antiallergic; mite; IgE;	382 DFKGHCQKPNLLNKNVHNMINGDEKNSFECILGPSTTTPTPTPTPTPTPTPTPTPTPT 441
KW	mite allergenic protein; immunoglobulin E; hypersensitivity;	
KW	immunocomplex formation.	383 DFKGHCQKPNLLNKNVHNMINGDEKNSVECLLGPSTTTPTPTPTPTPTPTPTPTPT 415
XX		
OS	Dermatophagoides farinae.	442 TTTPSPPT 501
XX		
PN	WO200222807-A2.	416 -----PTTDTSTSTPKYTYID 433
XX		
PD	21-MAR-2002.	502 GHLIKCYKEGDIPTPTNHNKLVCEFY---NGGWHVHIMPCPPGTINCOEKLTCIGE 555
XX		
PF	14-SEP-2001; 2001WO-US028730.	434 GHLIKCYKQGYLPPTDVHKYLVCEYIATPNGGWHVHIMDCPKGTRWHATLKNLCIQE 490
XX		
PR	14-SEP-2000; 2000US-00662293.	
XX	(HESK-) HESKA CORP.	
XX	McCall CA, Hunter SW, Weber ER;	
XX	WPI; 2002-351888/38.	
DR	N-PSDB; ABK69585.	
XX		
PT	New mite allergenic protein isolated from Dermatophagoides, designated	
PT	Der HMW-map protein, useful as a vaccine for treating mite allergy.	
XX		
PS	Claim 12; Page 144-146; 161pp; English.	
XX		
CC	The invention relates to an isolated mite allergenic protein of	
CC	Dermatophagoides, designated Der HMW-map protein, and its related nucleic	
CC	acid. The Der HMW-map protein is useful for eliciting an immune response	
CC	against Der HMW-map protein. The protein or a reagent comprising a non-	
CC	proteinaceous epitope is useful for identifying an animal (e.g., dog,	
CC	cat) susceptible to or having an allergic response to a mite. A	
CC	therapeutic composition is useful for desensitising a host animal to an	
CC	allergic response to a mite. The DNA and protein can be used in the	
CC	detection of anti-Der HMW-map antibodies in animal fluids, and inhibition	
CC	of immunoglobulin (Ig)E or Der HMW-map protein activity associated with a	
CC	disease. Antibodies that bind to Der HMW-map are useful for inhibiting	
CC	binding of proteins to IgE, to prevent immunocomplex formation, thus	
CC	reducing hypersensitivity responses to mite allergens, and as vaccines	
CC	against mite allergen hypersensitivity. Sequences AAU96314-AAU96342	
CC	represent Der HMW-map polypeptides of the invention	
XX		
SQ	Sequence 490 AA;	
	Query Match 79.7%; Score 2475; DB 5; Length 490;	
	Best Local Similarity 82.5%; Pred. No. 1.5e-171;	
	Matches 443; Conservative 21; Mismatches 21; Indels 52; Gaps 2;	
QY	22 KRDNHNSKNPWRIVCYGTWSVHKVDPTIEDIDPKCTHLMYGFADIKYKTIQVF 81	
DB	3 KRDNHNSKNPWRIVCYGTWSVHKVDPTIEDIDPKCTHLMYGFADIKYKTIQVF 62	
QY	82 DPYODNHSNMEKRGYERFNNLRNLPKLTWISLGGWYEGSEKYSMDAANPTVROQFIQ 141	
DB	63 DFPQDNHNSNMEKRGYERFNNLRNLPKLTWISLGGWYEGSEKYSMDAANPTVROQFVQ 122	
QY	142 SVLDFLOQYKFDGLDWEYFGPSRLGNPKIDKQNYLALVRELKDAFEPHYLLTAASVPG 201	
DB	123 SVLDFLOQYKFDGLDWEYFGPSRLGNPKIDKQNYLALVRELKDAFEPHYLLTAASVPG 182	
QY	202 KDKIDRAYDIKELNKLFWNNVWYDYGHWENFYGHNAPLYKRPDETDELHTFYNNYT 261	
DB	183 KDKIDVAYELKELNQLFDWNNVWYDYGHWENFYGHNAPLYKRPDETDELHTFYNNYT 242	

Fusion protein useful for combating insect pests, comprises a translocating moiety comprising a plant protein capable of acting as a carrier to translocate toxic moiety inside plant pathogen, and a toxic moiety.

Claim 7; Fig 15; 51pp; English.

The present sequence is that of the mosquito Anopheles gambiae chitinase.

CC This protein is used in claimed fusion proteins of the invention. Such
 CC fusion proteins comprise a translocating moiety and a toxic moiety, where
 CC the translocating moiety is a plant protein (e.g. a lectin) capable of
 CC acting as a carrier to translocate the toxic moiety across the gut wall
 CC of a plant pathogen, and the toxic moiety is an insect-derived peptide or
 CC protein capable of causing deleterious effects on growth, development,
 CC reproduction or mortality in pest insects. Suitable insect peptides and
 CC proteins include allatotaxins, chitinase, diuretic hormone and their
 CC metabolites and analogues. Polynucleotides encoding the fusion protein,
 CC vectors, host cells and transgenic plants that are resistant to disease
 CC are also provided. The fusion protein is target-specific, and resists
 CC degradation in the insect gut

SQ Sequence 525 AA;

Query Match 32.5%; Score 1008.5; DB 6; Length 525;
 Best Local Similarity 38.4%; Pred. No. 7.7e-65;
 Matches 211; Conservative 93; Mismatches 187; Indels 59; Gaps 13;

QY 8 LSIACIGLWNASIKRD-HNDYSKNPMRIVCVGTWMSYHKVD-PYTTIEDDPKCTHLM 65
 DB 5 VGVVLVVAFAAEFPHKASAEKGVVGVGTWAVYRPGNGRYDIEH-DPSLCTHLM 64
 QY 66 YGFAKIDEXYTIQVDPYQDDNHNHSEKRGYERFNNRLKNPELTMTISLGGWYEGSEK 125
 DB 65 YGFFGINE-DAVRIIDPYLDLEN-WRGHRIKRVGLXNVGPGKLTAAIGGWNESRK 122
 QY 126 YSDMAANPTTROOFTQSVLDF-QEYKFDGLDLDWEYPGSRGNPKIDKONYALVRELKD 185
 DB 123 PSMAASGELRKRFSIDCVAFQCRGHGFDGLDLDWEYPAQRDGNPLIDRDNAQLVEEMRE 182
 QY 186 APEPHGYLLTAAVSPGKKIDRAYDIKELNKLFDWNNVTYDYGWENFYGHNAPLYKR 245
 DB 183 EFDHYGLLLTAAVSVEFSAGVSYDIPRISKSFHFENVMVYDMHGAWDSYCGINAPLYRG 242
 QY 246 PDETDELHYTFNNVTMYLNNGTROKLVGVFPYGRANSIEDRSKLGDPKGMSP 305
 DB 243 SADTTDLRGQIWNVNAIHFWLAQGCTGRKLVGLIPLYGRNFTLASAANTQIGAPTVGGGT 302
 QY 306 PGFISGEEVGLSVIELCOLFOKEWHIOYDEVYNAIPYGVNDKIWVGVDLDSISCKLAPL 365
 DB 303 VGRYTRPGVWGYNEFECEKLAETAWDLWSEQQVYAVRNNQWVGYYDLSVQLKVYL 362
 QY 366 KELGVSGVMVWLENDDPKGHC-GPKNPLLNKHVNMINGDERKNSPECILGSTTTPTPT 424
 DB 363 LDQGLGAMVWSLETDDPLGVCGGGRYPUMHEIRSLVNGGT-----PSTTTPPSV 413
 QY 425 TPT 484
 DB 414 APTT-----STVAPGTTTPTTGANPGTTPPT--SDAPNHTTTSTTTTEGNPGTTRPPSG 466
 QY 485 TTEHTSETPKYTYVYDGLIKCY--KEGDIHPNTNHHKLYC-----EFVNGGWVH 535
 DB 467 -----DG---PCAGRGYGVFPHPTNCARYICTADTYEFT----- 500
 QY 536 IMPCPPGTIW 545
 DB 501 ---CPPGTLP 507

RESULT 12

ABB58595
 ID ABB58595 standard; protein; 4498 AA.
 XX
 AC ABB58595;
 XX
 DT 26-MAR-2002 (first entry)
 XX

DE Drosophila melanogaster polypeptide SEQ ID NO 2577.

XX Drosophila; developmental biology; cell signalling; insecticide;
 KW
 XX pharmaceutical.

OS Drosophila melanogaster.

XX WO200171042-A2.

XX 27-SEP-2001.

PD 23-MAR-2001; 2001WO-US009231.

XX 23-MAR-2000; 2000US-0191637P.

PR 11-JUL-2000; 2000US-00614150.

XX (PEKE) PE CORP NY.

XX Venter JC, Adams M, Li PWD, Myers EW;

XX WFI; 2001-656860/75.

DR N-PSDB; ABL02698.

XX New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signaling and cell-cell
 PT interactions.

XX Disclosure; SEQ ID NO 2577; 21pp + Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB5773-
 CC ABB72072). The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 4498 AA;

Query Match 27.5%; Score 854.5; DB 4; Length 4498;
 Best Local Similarity 33.8%; Pred. No. 2e-52;
 Matches 202; Conservative 88; Mismatches 188; Indels 119; Gaps 21;

QY 2 KTIYAIIISACIGLWNASIKRDHNDYSKNPMRIVCVGTWMSYH---KVDYPTTIEDID 57
 DB 33 QTLFLCALAYCI-----NEASSEG-RVVCYTTWMSYRPTGAKPNP---QNIN 77
 QY 58 PFKCTHLMY---GPAKIDEXYTIQVDPYQDDNHNHSEKRGYERFNNRLKNPELTMTI 114
 DB 78 PYLCTHUVYAFGGFTKDNQMK---PDKYQD-----IEGGYAKFTGLKTYNKQLKXTMI 128
 QY 115 SLGWSYEGSBKYSDMAANPTTROOFTQSVLDFLQEYKFDGLDLDWEYPGSRGNPKIDKQ 174
 DB 129 AIGGNWNASRFPSPLVASNERROQFIKNILKFLRQNHFDGIDLDWEYPAHREGSKSRDR 188
 QY 175 NYLALVRELKDAFEPHG-----YLLTAAVSPGKKIDRAYDIKELNKLFDWNNVTYD 227
 DB 189 NYAQVQVELRAEFPERAEAKTGRTELLTMAVPAGIEYIDKGYDVPKLYKLDWNFVLT 248
 QY 228 YHGGWENFYGHNAPLYKRDPDETDELHY---FNNVTMYLNNGTROKLVGVFPYGR 284
 DB 249 FHSSEFVSVAHHAFLYSL--EEDSEYNYDAELNIDYSIKYLLKAGADRDLKVLGIPTYGR 306
 QY 285 AWSIEDRSKLGKIDGPAKGMSPPGFISGEEVGLSVIELCOLFOKE-EWH-IQYDEVYNAIPY 342
 DB 307 SYTLINEESTELGAPAGPGEGQGDATREKGYLAYEICQTLKDDPEVTVVQPNVWMPY 366
 QY 343 GYNDKIWVGVDLDSISCKLAFKLKELGVSGVMVWLENDDPKGHC-GPKNPLLNKHVNM 401
 DB 367 AYRENQWVGVDDEAIVRKAEEVYVAQGLGGMFWAIDNDDFRGTCNGKPYPLIEAA---- 422
 QY 402 NGDEKNSFECILGSTTTPT 445
 DB 423 ----KEAMVEALGLGINEVAKPSGQPKPSRSRSDNASNRNRLNGKTEAPLSSRRPSATR 478

RESULT 15
ABP72619
ID ABP72
XX
AC ABP72
XX
DT 11-JU

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Db      111 KYSHMVAQSTRMSFIRSVVSLPKYDFDGLDLDWEYPGAADRGGSFSDKDFLYLVOEL 170
Qy      184 KDAF--EPHGILTAAVSPGOKIDRAYDIKELNKLFDWMNVMTYDIHGGWENFYGHNAP 241
Db      171 RRAFIIRVKGWELTAAPLANFRLMEGYHVPCLQELDAIHVMSYDLRGNWAGFADVHSP 230
Qy      242 LYKRPDETDELHTYFNVTMYHLYLANGATROKLVNMGVPPFYGRAMSIED----- 290
Db      231 LYKRPDHD-QWAYEKLNVNDGLHLWEKGCPSNKLVVVGIFPYGRSFTLSAGNNNYGLGTFI 289
Qy      291 RSKLKLGDPAKGMSPPGFISGEEGVLSTYIELCOLFOKEE--WHIOYDEYYNAPYGYNDKI 348
Db      290 NKEAGGDPAPYTNATGF-----WAYYEICTEVDKDDSGWTKKWDQCKCPYAYKGTQ 342
Qy      349 WUGYDDLASISCKLAFKLKELGVSGVMWSLENDDFKHCPCGNPLNKNVNNMINGDEKNS 408
Db      343 WUGYEDPRSVEIKONWIKQKGYLGAMTWAIDMDDFQGLCGEKNPLIKILHKMS----- 396
Qy      409 FECILGPSITTPPTTPTTPTT-----TTPTTPS-----PTTPTTTPSPTTPTTTPSP 456
Db      397 -----SYTVPPPHTEHTTPEWARPPSTPSPDPSGDPITPTTTAKPASTTKTKTKIT 449
Qy      457 TTPPTTPSPIT-----PTP-TTPTPAPTSTPSPTTTEHTSETPKYTYVVDGHLI 505
Db      450 TTTAKPPQGVDEENDINVRPEKPEPEPEVEVP-PTENE-----VDGSEI 497
Qy      506 KQYKGD-IPHPNTIHKYLVCEFNCGMWVHIMPCCPGTIWCQEKLT 552
Db      498 -CNSDQDIYIPDKKHCDKYWRC--VNGE--AMQFSCQHGTVFNVNLNVC 540

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Search completed: March 22, 2004, 06:51:46
 Job time : 169.752 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 22, 2004, 06:59:34 ; Search time 113.53 Seconds
(without alignments)
1265.926 Million cell updates/sec

Title: US-09-662-293-18

Perfect score: 3107
Sequence: 1 MKTIYAILSIMACIGLMNASIKRDNDYKPKMIRIVCVGTWSVYHKVDPTIEDIDPFK 60

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1049977 seqs, 258955339 residues

Total number of hits satisfying chosen parameters: 1049977

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database :
- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pcp.*
 - 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pcp.*
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 - 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pcp.*
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 - 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pcp.*
 - 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pcp.*
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 - 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pcp.*
 - 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pcp.*
 - 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pcp.*
 - 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3107	100.0	555	14	US-10-218-743-15
2	3107	100.0	555	14	US-10-218-743-18
3	3014	97.0	536	14	US-10-218-743-21
4	2542	81.8	509	14	US-10-218-743-35
5	2542	81.8	509	14	US-10-218-743-38
6	2475	79.7	490	14	US-10-218-743-41
7	738	23.8	485	14	US-10-004-2193-10
8	738	23.8	466	14	US-10-161-547-2
9	736.5	23.7	473	14	US-10-004-2193-4
10	732	23.6	466	14	US-10-161-547-4
11	729.5	23.5	452	14	US-10-004-2193-9
12	721.5	23.2	373	14	US-10-161-547-14
13	721.5	23.2	373	14	US-10-161-547-15
14	708.5	22.8	455	14	US-10-004-2193-14
15	708.5	22.8	476	14	US-10-004-2193-1

16	705.5	22.7	617	15	US-10-369-493-6743	Sequence 6743, Ap
17	668	21.5	678	15	US-10-295-027-6332	Sequence 632, App
18	662.5	21.3	457	15	US-10-094-749-1900	Sequence 1900, Ap
19	662	21.3	383	14	US-10-037-340-45	Sequence 45, Appl
20	662	21.3	383	15	US-10-235-027-270	Sequence 270, Appl
21	650	20.9	383	9	US-09-459-749D-17	Sequence 17, Appl
22	630	20.3	385	15	US-10-295-027-278	Sequence 278, App
23	630	20.3	423	15	US-10-373-802-2	Sequence 2, Appli
24	592	19.1	599	15	US-10-369-493-17162	Sequence 17162, A
25	521.5	16.8	407	15	US-10-369-493-20271	Sequence 20271, A
26	516	16.6	428	15	US-10-369-493-16644	Sequence 16644, A
27	471	15.2	392	15	US-10-369-493-19361	Sequence 19361, A
28	458	14.7	351	15	US-10-369-493-12478	Sequence 12478, A
29	438	14.1	366	12	US-10-424-599-209667	Sequence 209667, A
30	414.5	13.3	485	15	US-10-369-493-3399	Sequence 3399, Ap
31	406	13.1	371	9	US-09-923-844B-2	Sequence 2, Appli
32	405	13.0	546	15	US-10-369-493-18584	Sequence 18584, A
33	401.5	12.9	399	14	US-10-316-754-11	Sequence 11, Appl
34	401.5	12.9	399	14	US-10-316-754-19	Sequence 19, Appl
35	372.5	12.0	449	15	US-10-369-493-3308	Sequence 3308, Ap
36	367.5	11.8	511	15	US-10-369-493-1684	Sequence 1684, Ap
37	352.5	11.3	572	15	US-10-369-493-18585	Sequence 18585, A
38	350.5	11.3	358	12	US-10-425-114-47084	Sequence 47084, A
39	350.5	11.3	365	12	US-10-424-599-273219	Sequence 273219, A
40	347.5	11.2	567	15	US-10-369-493-8158	Sequence 8158, Ap
41	337	10.8	789	15	US-10-369-493-12804	Sequence 12804, A
42	329.5	10.6	445	15	US-10-369-493-3089	Sequence 3089, Ap
43	317.5	10.2	462	15	US-10-369-493-8244	Sequence 8244, Ap
44	314	10.1	432	15	US-10-369-493-5521	Sequence 5521, Ap
45	313.5	10.1	607	14	US-10-156-761-10415	Sequence 10415, A

ALIGNMENTS

RESULT 1

US-10-218-743-15
; Sequence 15, Application US/10218743
; Publication No. US20030096779A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/10/218,743
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/09/292,225
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: 60/098,909
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/085,295
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/098,565
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: 09/062,013
; PRIOR FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 555
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-10-218-743-15

Query Match 100.0%; Score 3107; DB 14; Length 555;
Best Local Similarity 100.0%; Pred. No. 3e-220;
Matches 555; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKTIYAILSIMACIGLMNASIKRDNDYKPKMIRIVCVGTWSVYHKVDPTIEDIDPFK 60
Db 1 MKTIYAILSIMACIGLMNASIKRDNDYKPKMIRIVCVGTWSVYHKVDPTIEDIDPFK 60

QY 61 CTHLMYGFPAKIDYKTYIQVDFPYQDDNHNSEKGYERFNNLRKLNKPELTMTMISLGWY 120
Db 61 CTHLMYGFPAKIDYKTYIQVDFPYQDDNHNSEKGYERFNNLRKLNKPELTMTMISLGWY 120
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Db 121 EGSEKYSDMAANPTVRQOFIQSVLDFLOEYKFDGLDWEYFGSLGNPKIDKQNYLALV 180
QY 181 RELKDAFEPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYGHWENFYGHNA 240
Db 181 RELKDAFEPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYGHWENFYGHNA 240
QY 241 PLYKRDETDDELHTYFNNVNTMHHYLLNNGATRDKLVGMVFPFYGRAWSIEDRSKLGDPGA 300
Db 241 PLYKRDETDDELHTYFNNVNTMHHYLLNNGATRDKLVGMVFPFYGRAWSIEDRSKLGDPGA 300
QY 301 KGMSPPGFISSGEGVLSYIELCOLFOKEEWHIQYDEYVNAFYNDKLVGMVFPFYGRAWSIEDRSKLGDPGA 360
Db 301 KGMSPPGFISSGEGVLSYIELCOLFOKEEWHIQYDEYVNAFYNDKLVGMVFPFYGRAWSIEDRSKLGDPGA 360
QY 361 KLAFLKELGSGVGMVWSLENDDFKHCCKPKNPLLNKVNHNMGDEKNSFECILGSPSTTTP 420
Db 361 KLAFLKELGSGVGMVWSLENDDFKHCCKPKNPLLNKVNHNMGDEKNSFECILGSPSTTTP 420
QY 421 TPSTTTTHTSETPKYTYVVDGHLIKCYKEGDIHPHTNIHKLVCEVNGGWWHIMPCP 540
Db 421 TPSTTTTHTSETPKYTYVVDGHLIKCYKEGDIHPHTNIHKLVCEVNGGWWHIMPCP 540
QY 541 PGTWCQEKLTICGE 555
Db 541 PGTWCQEKLTICGE 555

RESULT 2
US-10-218-743-18
; Sequence 18, Application US/10218743
; Publication No. US20030096779A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/10/218,743
; PRIOR FILING DATE: 2002-08-13
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: 60/098,909
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/085,295
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085,295
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: 60/098,565
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: 09/062,013
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 18
; LENGTH: 555
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-10-218-743-18

Query Match 100.0%; Score 3107; DB 14; Length 555;
Best Local Similarity 100.0%; Pred. No. 3e-220;
Matches 555; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKTIYAILSIACIGLNMNASIKRDNDYSKNPNRIVCYVGTWVSVYHKVDPYTTIEDIDPPK 60
Db 1 MKTIYAILSIACIGLNMNASIKRDNDYSKNPNRIVCYVGTWVSVYHKVDPYTTIEDIDPPK 60
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QY 121 EGSEKYSDMAANPTVRQOFIQSVLDFLOEYKFDGLDWEYFGSLGNPKIDKQNYLALV 180
Db 121 EGSEKYSDMAANPTVRQOFIQSVLDFLOEYKFDGLDWEYFGSLGNPKIDKQNYLALV 180
QY 181 RELKDAFEPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYGHWENFYGHNA 240
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QY 241 PLYKRDETDDELHTYFNNVNTMHHYLLNNGATRDKLVGMVFPFYGRAWSIEDRSKLGDPGA 300
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Db 301 KGMSPPGFISSGEGVLSYIELCOLFOKEEWHIQYDEYVNAFYNDKLVGMVFPFYGRAWSIEDRSKLGDPGA 360
QY 361 KLAFLKELGSGVGMVWSLENDDFKHCCKPKNPLLNKVNHNMGDEKNSFECILGSPSTTTP 420
Db 361 KLAFLKELGSGVGMVWSLENDDFKHCCKPKNPLLNKVNHNMGDEKNSFECILGSPSTTTP 420
QY 421 TPSTTTTHTSETPKYTYVVDGHLIKCYKEGDIHPHTNIHKLVCEVNGGWWHIMPCP 540
Db 421 TPSTTTTHTSETPKYTYVVDGHLIKCYKEGDIHPHTNIHKLVCEVNGGWWHIMPCP 540
QY 541 PGTWCQEKLTICGE 555
Db 541 PGTWCQEKLTICGE 555

RESULT 3
US-10-218-743-21
; Sequence 21, Application US/10218743
; Publication No. US20030096779A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/10/218,743
; PRIOR FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/09/292,225
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: 60/098,909
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/085,295
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085,295
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: 09/062,013
; PRIOR FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 21
; LENGTH: 536
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-10-218-743-21

Query Match 97.0%; Score 3014; DB 14; Length 536;

Best Local Similarity 100.0%; Pred. No. 2e-213; Matches 536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 121 IQSVLDFLOEYKFDGLDWEYFGSLNPKIDKQNYLALVRELKDAFPHGYLLTAAYS 180

QY 200 PGKDKIDRAYDIKELNKLFDMMNVMTYDHYGGWENFYGNAPLYKRPDETDELHTYFNVN 259
Db 181 PGKDKIDRAYDIKELNKLFDMMNVMTYDHYGGWENFYGNAPLYKRPDETDELHTYFNVN 240

QY 260 YTHVYLNNGATRDKLVMGVFFYGRAWSIEDRSKLGDPAGKMSPPGFIISGEGVLSYI 319
Db 241 YTHVYLNNGATRDKLVMGVFFYGRAWSIEDRSKLGDPAGKMSPPGFIISGEGVLSYI 300

QY 320 ELCQLFQKEBWHIOYDEYNNAPYGYNDKIWVGDDLASISCKLAFKELGVSGVMWWSLE 379
Db 301 ELCQLFQKEBWHIOYDEYNNAPYGYNDKIWVGDDLASISCKLAFKELGVSGVMWWSLE 360

QY 380 NDFKHCGBGKPNLLKVNMMINGDEKNSPECILGPSTTTPTTPTTPTTPTTPTTPTTPT 439
Db 361 NDFKHCGBGKPNLLKVNMMINGDEKNSPECILGPSTTTPTTPTTPTTPTTPTTPTTPT 420

QY 440 TPT 499
Db 421 TPT 480

QY 500 VDGLHKYCKEGBDIPHTNIHKYLVCFVNGVWVHIMPCPGTIWCQEKLCIG 555
Db 481 VDGLHKYCKEGBDIPHTNIHKYLVCFVNGVWVHIMPCPGTIWCQEKLCIG 536

RESULT 4
US-10-218-743-35
; Sequence 35, Application US/10218743
; Publication No. US20030096779A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/10/218,743
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/09/292,225
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: 60/098,909
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/085,295
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/098,565
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: 09/062,013
; PRIOR FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 35
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-10-218-743-35

Query Match 81.8%; Score 2542; DB 14; Length 509;
Best Local Similarity 81.7%; Pred. No. 1e-178;

Matches 456; Conservative 24; Mismatches 26; Indels 52; Gaps 2;

QY 1 MKTYAILUSIMACIGLMMNASIKRDHNDYSKNPMRIVCVYGVTSVYHKVDPTTIEDDPFK 60
Db 1 MKTYPALFCIWACIGLMMNAATKRDHNDYSKNPMRIVCVYGVTSVYHKVDPTTIEDDPFK 60

QY 61 CTHLMYGFADIEYKTYIQVDPYODDHNHSEKRGYERFNNLRKLNPELTMTISLGWY 120
Db 61 CTHLMYGFADIEYKTYIQVDPYODDHNHSEKRGYERFNNLRKLNPELTMTISLGWY 120

QY 121 EGSEKYSMAANPTTQROFIOQSVLDFLOEYKFDGLDWEYFGSLNPKIDKQNYLALV 180
Db 121 EGSEKYSMAANPTTQROFIOQSVLDFLOEYKFDGLDWEYFGSLNPKIDKQNYLALV 180

QY 181 RELKDAFPHGYLLTAAYSPGKDKIDRAYDIKELNKLFDMMNVMTYDHYGGWENFYGNNA 240
Db 181 RELKDAFPHGYLLTAAYSPGKDKIDRAYDIKELNKLFDMMNVMTYDHYGGWENFYGNNA 240

QY 241 PLYKRPDETDELHTYFNVNMTYDHYGGWENFYGNAPLYKRPDETDELHTYFNVN 300
Db 241 PLYKRPDETDELHTYFNVNMTYDHYGGWENFYGNAPLYKRPDETDELHTYFNVN 300

QY 301 KGMSPPGFISGEGVLSYIELCQLFQKEBWHIOYDEYNNAPYGYNDKIWVGDDLASISC 360
Db 301 KGMSPPGFISGEGVLSYIELCQLFQKEBWHIOYDEYNNAPYGYNDKIWVGDDLASISC 360

QY 361 KLAFLKELGVSGVMWWSLENDDEKHCGBGKPNLLKVNMMINGDEKNSPECILGPSTTPT 420
Db 361 KLAFLKELGVSGVMWWSLENDDEKHCGBGKPNLLKVNMMINGDEKNSPECILGPSTTPT 420

QY 421 TPT 480
Db 421 TPT 434

QY 481 TPT 537
Db 435 ---PTTDSYSETPKYTYIDGHLIKYCKEGBDIPHTNIHKYLVCFV---NGWVWVHIM 491

QY 538 PCPGTIWCQEKLCIG 555
Db 492 DCPKTRWHTATLKNCIOE 509

RESULT 5
US-10-218-743-38
; Sequence 38, Application US/10218743
; Publication No. US20030096779A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/10/218,743
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/09/292,225
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: 60/098,909
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/085,295
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/098,565
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: 09/062,013
; PRIOR FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 38
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-10-218-743-38

Query Match 81.8%; Score 2542; DB 14; Length 509;
Best Local Similarity 81.7%; Pred. No. 1e-178;
Matches 456; Conservative 24; Mismatches 26; Indels 52; Gaps 2;

1 MKTIVAILISACIGLMAASIKRDHNDYSKPMRIVCVGTWVYHKVDPYTIIDDPFK 60
1 MKTIFALFCIWACIGLMAAARKDHNYSKPMRIVCVGTWVYHKVDPYTIIDDPFK 60
61 CTHLMYGFPAKIDYKTYIQVDPYQDDNNHNSWKGVERFNNLRLKNPELTMTISLGWY 120
61 CTHLMYGFPAKIDYKTYIQVDPYQDDNNHNSWKGVERFNNLRLKNPELTMTISLGWY 120
121 EGSEKYSMAANPTVROQFIQSVDLFLQYKFDGLDLDWEYPSGLGNPKIDKQNYLTV 180
121 EGSEKYSMAANPTVROQFIQSVDLFLQYKFDGLDLDWEYPSGLGNPKIDKQNYLTV 180
181 RELKDAEPHGVLLTAAYSPGKIDRAVDIKELNKLFDWMNVMTYDYGHWENFYGHNA 240
181 RELKEAFBFFGVLTAAYSPGKIDRAVDIKELNKLFDWMNVMTYDYGHWENFYGHNA 240
241 PLYKGPDETDLHTYFNNVNTYHYYLNGATRDKLVMGVPFYGRAWSIEDRSKVLGDDPA 300
241 PLYKGPDETDLHTYFNNVNTYHYYLNGATRDKLVMGVPFYGRAWSIEDRSKVLGDDPA 300
301 KMSPPGISGEGVLSVIELCOLFQKEWHIOYDEYNNAPYGYNDKLVWGYDDIASISC 360
301 KMSPPGISGEGVLSVIELCOLFQKEWHIOYDEYNNAPYGYNDKLVWGYDDIASISC 360
361 KLAFKELGVSGVWVWSLENDDFKHGCGPKPLNKNVHNMINGDEKNSFCILGPSTTP 420
361 KLAFKELGVSGVWVWSLENDDFKHGCGPKPLNKNVHNMINGDEKNSFCILGPSTTP 420
421 PTTTST 480
421 PTTTST 480
481 TPSPPTTST 537
435 ---PTTST 555
538 PCPPGTINQCEKLTICGE 555
492 DCPKGRWHTATLKNKICQE 509

RESULT 6
US-10-218-743-41
; Sequence 41, Application US/10218743
; Publication No. US20030096779A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/10/218,743
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/09/292,225
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: 60/098,909
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/085,295
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/098,565
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: 09/062,013
; PRIOR FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 41
; LENGTH: 490

TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-10-218-743-41

Query Match 79.7%; Score 2475; DB 14; Length 490;
Best Local Similarity 82.5%; Pred. No. 8.4e-174;
Matches 443; Conservative 21; Mismatches 21; Indels 52; Gaps 2;

22 KRDHNDYSKPMRIVCVGTWVYHKVDPYTIIDDPFKCTHLMYGFPAKIDYKTYIQV 81
3 KRDHNDYSKPMRIVCVGTWVYHKVDPYTIIDDPFKCTHLMYGFPAKIDYKTYIQV 82
82 DPYQDDNNHNSWKGVERFNNLRLKNPELTMTISLGWYEGSEKYSMAANPTVROQFIQ 141
63 DPYQDDNNHNSWKGVERFNNLRLKNPELTMTISLGWYEGSEKYSMAANPTVROQFIQ 122
142 SVLDLFLQYKFDGLDLDWEYPSGLGNPKIDKQNYLTVRELKEAFBFFGVLTAAYSPG 182
123 SVLDLFLQYKFDGLDLDWEYPSGLGNPKIDKQNYLTVRELKEAFBFFGVLTAAYSPG 182
202 KDKIDRAYDIKELNKLFDWMNVMTYDYGHWENFYGHNAPLYKRPDETDLHTYFNNVNT 261
183 KDKIDVAYELKELNQLFDWMNVMTYDYGHWENFYGHNAPLYKRPDETDLHTYFNNVNT 242
262 MHTYLANGATRDKLVMGVPFYGRAWSIEDRSKVLGDDPAKGMSPPGFISGEGVLSYIEL 321
243 MHTYLANGATRDKLVMGVPFYGRAWSIEDRSKVLGDDPAKGMSPPGFISGEGVLSYIEL 302
322 COLFQKEWHIOYDEYNNAPYGYNDKLVWGYDDIASISCKLAFKELGVSGVWVWSLEND 381
303 COLFQKEWHIOYDEYNNAPYGYNDKLVWGYDDIASISCKLAFKELGVSGVWVWSLEND 362
382 DFKHGCGPKPLNKNVHNMINGDEKNSFCILGPSTSTPTPTPTPTPTPTPTPTPTPT 441
363 DFKHGCGPKPLNKNVHNMINGDEKNSFCILGPSTSTPTPTPTPTPTPTPTPTPTPT 415
442 TTTTST 501
416 -----PTTSTSTSTPT 433
502 GHLIKYKQYGLPHTDVKHLYVCEYIAIPNGGWWHIMDCPKGRWHTATLKNKICQE 555
434 GHLIKYKQYGLPHTDVKHLYVCEYIAIPNGGWWHIMDCPKGRWHTATLKNKICQE 490

RESULT 7
US-10-004-219B-10
; Sequence 10, Application US/10004219B
; Publication No. US20030087414A1
; GENERAL INFORMATION:
; APPLICANT: Macrozyme
; APPLICANT: Aerts, Johannes M.F.G.
; APPLICANT: Boot, Rolf G.
; TITLE OF INVENTION: A mammalian mucinase, its recombinant production, and
; TITLE OF INVENTION: its use in therapy or prophylaxis against diseases in
; TITLE OF INVENTION: which mucus is involved or infection diseases
; FILE REFERENCE: 2183-5136US
; CURRENT APPLICATION NUMBER: US/10/004,219B
; CURRENT FILING DATE: 2001-11-02
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(445)
; OTHER INFORMATION: /note="Human chitotriosidase"
US-10-004-219B-10

Query Match 23.8%; Score 738; DB 14; Length 445;
Best Local Similarity 34.2%; Pred. No. 5.3e-46;

Matches	152;	Conservative	85;	Mismatches	150;	Indels	58;	Gaps	11;
QY	34	RIVCYVGTWSVYHKVDP--YTIEDIDPPKCTHLMYGFAKIDEYKYTIQVFDPPYQDDNNHNSW	92						
Db	2	KLVCYFTNWAQYRQGEARFLPKDLDPSLCTHLIYAFAGMTHQLST-----TEW	50						
QY	93	-EKRGYERFNNLRKNKPELTMTISLGWYGESEKYSDMAANPTYRQOFTQSVLDFLOEYK	151						
Db	51	NDETLVQEFNGLKQWPKLKTLLAIGGNFQKFTDMVATANNRQTFVNSAIRFLRKYS	110						
QY	152	FDGLDLDWEYPGSRIGNPKIDKQNYLAVRELKDAFEPHG-----YLLTAAVSPGDK	204						
Db	111	FDGLDLDWEYPGSG--GSPAVDKERFTTLVDLANAFOQEAQTSGERLLLSAAPAGQTY	169						
QY	205	IDRAYDIKELNKLFDMMNVMTYDHYGGWENFYGHNAPLYRKPDETDELHTYFNWNYTMHY	264						
Db	170	VDAGYEVDKIAQNLDFVNLMAIDPHGSEKVTGHNSFLYKROESGAAS--LNVDAAVQQ	228						
QY	265	YLNNGATRDKLVWGVPFFYGRAWSIEDRSKCLKGDPAKGMSPPGFIAGEGVLSTYELCQL	324						
Db	229	WLQKTPASKLILGHPYTGRTTGLASSDSRTRVGAPATGSGTPGPTKGGMLAYEVCWS	288						
QY	325	FOKEEWHIQDYDEYNAPYGYNDKIWGVYDDLIASISCKLAFLKBLGSGVWVMSLENDPDK	384						
Db	289	KGATKRIQ-DQ--KVPIYFRDNQWGFDDVSEFKTVSVLKQKGLGGAWWALDLDFA	345						
QY	385	GHCGPKNPLLNKVHNMINGDEKNFECILGSGTTTTPTPTPTPTPTPTPTPTPTPTPTPT	444						
Db	346	G-----FSCNQG-----RYPLIQTLRQELSPLVLPST	373						
QY	445	PSPT	469						
Db	374	PELEVP-KPGQSPSEPHGSPSQDT	397						
RESULT 8									
US-10-161-547-2									
; Sequence 2, Application US/10161547									
; Publication No. US20030143216A1									
; GENERAL INFORMATION:									
; APPLICANT: Gray, Patrick W.									
; APPLICANT: Tjoelker, Larry W.									
; TITLE OF INVENTION: CHITINASE CHITINASE-BINDING FRAGMENTS									
; FILE REFERENCE: 27866/35407									
; CURRENT APPLICATION NUMBER: US/10/161,547									
; CURRENT FILING DATE: 2002-06-03									
; PRIOR APPLICATION NUMBER: US/09/267,574									
; PRIOR FILING DATE: 1999-03-12									
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/039,198									
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-03-12									
; NUMBER OF SEQ ID NOS: 39									
; SOFTWARE: PatentIn Ver. 2.0									
; SEQ ID NO 2									
; LENGTH: 466									
; TYPE: PRT									
; ORGANISM: Homo sapiens									
US-10-161-547-2									
Query Match 23.8%; Score 738; DB 14; Length 466;									
Best Local Similarity 34.2%; Pred. No. 5.6e-46;									
Matches 152; Conservative 85; Mismatches 150; Indels 58; Gaps 11									
QY	34	RIVCYVGTWSVYHKVDP--YTIEDIDPPKCTHLMYGFAKIDEYKYTIQVFDPPYQDDNNHNSW	92						
Db	23	KLVCYFTNWAQYRQGEARFLPKDLDPSLCTHLIYAFAGMTHQLST-----TEW	71						
QY	93	-EKRGYERFNNLRKNKPELTMTISLGWYGESEKYSDMAANPTYRQOFTQSVLDFLOEYK	151						
Db	72	NDETLVQEFNGLKQWPKLKTLLAIGGNFQKFTDMVATANNRQTFVNSAIRFLRKYS	131						
QY	152	FDGLDLDWEYPGSRIGNPKIDKQNYLAVRELKDAFEPHG-----YLLTAAVSPGDK	204						
Db	132	FDGLDLDWEYPGSG--GSPAVDKERFTTLVDLANAFOQEAQTSGERLLLSAAPAGQTY	190						


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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 373
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-161-547-14

Query Match      23.2%; Score 721.5; DB 14; Length 373;
Best Local Similarity 37.7%; Pred. No. 6.9e-45;
Matches 136; Conservative 83; Mismatches 117; Indels 25; Gaps 8;

QY 34 RIVCYVGTWSVYHKVDP-YTIEDIDPFKCTHLMYGFADKIDVYKTIQVDFPYQDDNHSW 92
Db 2 KLVCYFTNWAQYRQGEARFPLKDLPSLCTHLIYAFAGMTHQST-----TEW 50
QY 93 -EKRGYERFNRLRNKLPETLTMISLGGWYEGSEKYSMDAANPYRQOFTQSVLDLQYK 151
Db 51 NDETLVQEFNGLKQNPCKLITLLAIGGNWFGTKFTDMVATANNRQTFVNSAIRFLKYS 110
QY 152 FDGLDLDWEYPGSRIGLNPKIDKQNYLALVRELKDAFEPHG-----YLLTAASVPGDK 204
Db 111 FDGLDLDWEYPGSQ-GSPAVDKERFTTLVQDLANAFQQAQTSKGERILLLSAAVPAGQTY 169
QY 205 IDRAYDIKELNKLFDWMNVMYDYGWENFYGHNAPLYKRPDDETLHTYFNVTMHY 264
Db 170 VDAGYEVDKTAQNLDVFNLMAYDFHGSWEKVTGHSNPLYKQESGAAS-LNVDAAVQ 228
QY 265 YLNGATRDKLVMGVFFYGRAWSIEDRSKLGDPAGKMSPPGFISGEGVLSYELCOL 324
Db 229 WLQGTGTPASKILGMPTVGRSFTLASSSDTRVGAPATGSGTGPFTKEGGLAYEVCWS 288
QY 325 FQKEEWHIQYDEVYNAPYGYNDKIWVGVDYDLASISCKLAFKLKELGVSVMVMSLENDDFK 384
Db 289 KGATKQRIQ-DQ--KVPYIFPDNQWVGFDVSEFKTKVSYLKQKGLGGAMWALDLDFA 345
QY 385 G 385
Db 346 G 346

RESULT 14
US-10-004-219B-14
; Sequence 14, Application US/10004219B
; Publication No. US20030087414A1
; GENERAL INFORMATION:
; APPLICANT: Macrozyme
; APPLICANT: Aerts, Johannes M.F.G.
; APPLICANT: Boot, Rolf G.
; TITLE OF INVENTION: A mammalian mucinase, its recombinant production, and
; TITLE OF INVENTION: its use in therapy or prophylaxis against diseases in
; TITLE OF INVENTION: which mucus is involved or infection diseases
; FILE REFERENCE: 2183-5136US
; CURRENT APPLICATION NUMBER: US/10/004,219B
; CURRENT FILING DATE: 2001-11-02
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(455)
; OTHER INFORMATION: /note="Human AMCase"
US-10-004-219B-14

Query Match      22.8%; Score 708.5; DB 14; Length 455;
Best Local Similarity 35.9%; Pred. No. 8.1e-44;
Matches 149; Conservative 75; Mismatches 154; Indels 37; Gaps 10;

QY 34 RIVCYVGTWSVYHK-VDPYTIETIDPFKCTHLMYGFADKIDVYKTIQVDFPYQDDNHSW 92
Db 2 QLTCTYTNWAQYRPGLGFRFPNDIDPCLTCLHLIYAFAGRONNEIT-----TEW 50
QY 93 -EKRGYERFNRLRNKLPETLTMISLGGWYEGSEKYSMDAANPYRQOFTQSVLDLQYK 151
Db 51 NDETLVQEFNGLKQNPCKLITLLAIGGNWFGTKFTDMVATANNRQTFVNSAIRFLKYS 110
QY 152 FDGLDLDWEYPGSRIGLNPKIDKQNYLALVRELKDAFEPHG-----YLLTAASVPGDK 204
Db 111 FDGLDLDWEYPGSR-GSPPDQKHLFTVLVQEMREAEQKQINPKPLMWTAAVAAGISN 169
QY 205 IDRAYDIKELNKLFDWMNVMYDYGWENFYGHNAPLYKRPDDETLHTYFNVTMHY 264
Db 170 IQSGYEIPQLSQYLDYIHMVTYDLHGSWEKVTGHSNPLYKQESGAAS-LNVDAAVQ 228
QY 265 YLNGATRDKLVMGVFFYGRAWSIEDRSKLGDPAGKMSPPGFISGEGVLSYELCOL 324
Db 229 WKDNGAPAEKLVGPFYTHGNFILNSPTGTGAGTSGAGPAGPYAKSGGIWAYEIC-T 287
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QY 325 FQKEWHIQDEYYNAPYNDKIWGVYDDLASISCKLAFKELGVLGSGVMVWSLENDDEFK 384
Db 288 FLKNGATCGWDAPQEVYAYQGVWVYDNIKSFDDIAQWLKHNKFCGAMVWALDDFT 347
QY 385 G-HCGP-KNPLLNKVNMMINGDEKNSPECILGSPSTTTPTTPTTPTTPTTPTT 437
Db 348 GTFCNQGKFLI-----STLKKALGLQSASCTAPAQPIETITAAPSGS 390

RESULT 15
US-10-004-219B-1
; Sequence 1, Application US/10004219B
; Publication No. US20030087414A1
; GENERAL INFORMATION:
; APPLICANT: Macrozyme
; APPLICANT: Aerts, Rolf G.
; APPLICANT: Boot, Rolf G.
; TITLE OF INVENTION: A mammalian mucinase, its recombinant production, and
; TITLE OF INVENTION: its use in therapy or prophylaxis against diseases in
; TITLE OF INVENTION: which mucus is involved or infection diseases
; FILE REFERENCE: 2193-5136US
; CURRENT APPLICATION NUMBER: US/10/004,219B
; CURRENT FILING DATE: 2001-11-02
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: human AMCase
; OTHER INFORMATION: amino acid sequence deduced from cDNA sequence
US-10-004-219B-1

Query Match 22.8%; Score 708.5; DB 14; Length 476;
Best Local Similarity 35.9%; Pred. No. 8.6e-44;
Matches 149; Conservative 75; Mismatches 154; Indels 37; Gaps 10;

QY 34 RIVCVGVGWSVYHK-VDPYTIEDIDPFKCTHLMYGFAKIDBYKYTIQVDFPYQDDNHSW 92
Db 23 QLTCTFTWQAQYRPGUGRFMPDNIDPCLCTHLIYAFAGRQNEITT-----IEW 71
QY 93 -EKRGYERFNNLRNLKPELTMTMISGGWYEGSEKYSMDAANPTYRQQFIQSVLDFLOEYK 151
Db 72 NDTVLYQAFNGLKNKNSQLKTLAIGGNWFGTAPTAMVSTPENRQTFTSVIXFLRQYE 131
QY 152 FDGLDLDWEYPCSRIGNPKIDKQNYALVRELKDAPEPHG-----YLLTAAYSPGKDX 204
Db 132 FDGLDFDWEYPGSR-GSPPDQKHLFTVLVQENREAFQEAQINKPRLMWTAAVAAGISN 190
QY 205 IDRAYDIKELNKLFDWMVMTYDHYGGWENFYGHNAPLYKRPDETDELHLYFNVNYTWHY 264
Db 191 IQSGYEIPQLSQYLDYIHVMTYDLHGSWEGYTGENSEPLYKYPTDTGS-NAYLNVDYVWNY 249
QY 265 YLNNGATRDKLVMGVPPFYGRAMSIEDRSKLGIDPAKGMSPPGFTSGEGVLSYIELCOL 324
Db 250 WKDNGAPAEKLVGPTTYGHNFILNPSNTGIGAPTSAGAPAGPYAKESGIWAYYEIC-T 308
QY 325 FQKEWHIQDEYYNAPYNDKIWGVYDDLASISCKLAFKELGVLGSGVMVWSLENDDEFK 384
Db 309 FLKNGATCGWDAPQEVYAYQGVWVYDNIKSFDDIAQWLKHNKFCGAMVWALDDFT 368
QY 385 G-HCGP-KNPLLNKVNMMINGDEKNSPECILGSPSTTTPTTPTTPTTPTTPTT 437
Db 369 GTFCNQGKFLI-----STLKKALGLQSASCTAPAQPIETITAAPSGS 411
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Search completed: March 22, 2004, 07:45:52
Job time : 114.53 secs

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QM protein - protein search, using sw model

Run on: March 22, 2004, 06:59:34 ; Search time 109.643 Seconds
(without alignments)
1265.926 Million cell updates/sec

Title: US-09-662-293-21

Perfect score: 3014

Sequence: 1 SIKRDNYSKPMRIVCVV.....IMPCPGTTCOEKLTICGE 536

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1049577 seqs, 25895339 residues

Total number of hits satisfying chosen parameters: 1049577

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:

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- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3014	100.0	536	14	US-10-218-743-21
2	3014	100.0	555	14	US-10-218-743-15
3	3014	100.0	555	14	US-10-218-743-18
4	2475	82.1	490	14	US-10-218-743-41
5	2475	82.1	509	14	US-10-218-743-35
6	2475	82.1	509	14	US-10-218-743-38
7	738	24.5	445	14	US-10-004-219B-10
8	738	24.5	466	14	US-10-161-547-2
9	732	24.3	466	14	US-10-161-547-4
10	729.5	24.2	452	14	US-10-004-219B-9
11	729.5	24.2	473	14	US-10-004-219B-4
12	721.5	23.9	373	14	US-10-161-547-14
13	721.5	23.9	373	14	US-10-161-547-15
14	708.5	23.5	455	14	US-10-004-219B-14
15	708.5	23.5	476	14	US-10-004-219B-1

16	705.5	23.4	617	15	US-10-369-493-6743	Sequence 6743, Ap
17	667.5	22.1	678	15	US-10-295-027-632	Sequence 632, Ap
18	662.5	22.0	457	15	US-10-094-749-1900	Sequence 1900, Ap
19	660	21.9	383	14	US-10-097-340-45	Sequence 45, Appl
20	660	21.9	383	15	US-10-295-027-270	Sequence 270, Appl
21	650	21.6	383	9	US-09-459-749D-17	Sequence 17, Appl
22	630	20.9	385	15	US-10-295-027-278	Sequence 278, App
23	630	20.9	423	15	US-10-373-802-2	Sequence 2, Appli
24	588	19.5	599	15	US-10-369-493-17162	Sequence 17162, A
25	521.5	17.3	407	15	US-10-369-493-20271	Sequence 20271, A
26	516	17.1	428	15	US-10-369-493-16644	Sequence 16644, A
27	471	15.6	392	15	US-10-369-493-19361	Sequence 19361, A
28	458	15.2	351	15	US-10-369-493-12478	Sequence 12478, A
29	434.5	14.4	366	12	US-10-424-599-209667	Sequence 209667,
30	414.5	13.8	485	15	US-10-369-493-3399	Sequence 3399, Ap
31	406	13.5	371	9	US-09-923-844B-2	Sequence 2, Appli
32	405	13.4	546	15	US-10-369-493-18584	Sequence 18584, A
33	401.5	13.3	399	14	US-10-316-754-11	Sequence 11, Appl
34	401.5	13.3	399	14	US-10-316-754-19	Sequence 19, Appl
35	372.5	12.4	449	15	US-10-369-493-3308	Sequence 3308, Ap
36	367.5	12.2	511	15	US-10-369-493-1684	Sequence 1684, Ap
37	352.5	11.7	572	15	US-10-369-493-18585	Sequence 18585, A
38	350.5	11.6	358	12	US-10-425-114-47084	Sequence 47084, A
39	350.5	11.6	365	12	US-10-424-599-273219	Sequence 273219,
40	347.5	11.5	567	15	US-10-369-493-8158	Sequence 8158, Ap
41	337	11.2	789	15	US-10-369-493-12804	Sequence 12804, A
42	329.5	10.9	445	15	US-10-369-493-3089	Sequence 3089, Ap
43	317.5	10.5	462	15	US-10-369-493-8244	Sequence 8244, Ap
44	313.5	10.4	607	14	US-10-156-761-10415	Sequence 10415, A
45	311.5	10.3	427	14	US-10-156-761-14446	Sequence 14446, A

ALIGNMENTS

RESULT 1

US-10-218-743-21
; Sequence 21, Application US/10218743
; Publication No. US20030096779A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/10/218,743
; PRIOR FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/09/292,225
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: 60/098,909
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/085,295
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/098,565
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: 09/062,013
; PRIOR FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 536
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-10-218-743-21

Query Match 100.0%; Score 3014; DB 14; Length 536;
Best Local Similarity 100.0%; Pred. No. 1.2e-212;
Matches 536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SIKRDNYSKPMRIVCVVGVVYVVDPTTIEDIDPFKCTHLMYGFADIKYTIQ 60
Db 1 SIKRDNYSKPMRIVCVVYVYVVDPTTIEDIDPFKCTHLMYGFADIKYTIQ 60

[illegible]

RESULT 2

US-10-218-743-15

; Sequence 15, Application US/10218743

; Publication No. US20030096779A1

; GENERAL INFORMATION:

; APPLICANT: McCall, Catherine A.

; APPLICANT: Hunter, Shirley Wu

; APPLICANT: Weber, Eric R.

; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS

; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS

; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS

; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS

; FILE REFERENCE: AL-2-C3

; CURRENT APPLICATION NUMBER: US/10/218,743

; CURRENT FILING DATE: 2002-08-13

; PRIOR APPLICATION NUMBER: US/09/292,225

; PRIOR FILING DATE: 1999-04-15

; PRIOR APPLICATION NUMBER: 60/098,909

; PRIOR FILING DATE: 1998-09-02

; PRIOR APPLICATION NUMBER: 60/085,295

; PRIOR FILING DATE: 1998-05-13

; PRIOR APPLICATION NUMBER: 60/098,565

; PRIOR FILING DATE: 1998-04-17

; PRIOR APPLICATION NUMBER: 09/062,013

; PRIOR FILING DATE: 1998-04-17

; NUMBER OF SEQ ID NOS: 49

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 15

; LENGTH: 555

; TYPE: PRT

; ORGANISM: Dermatophagoides farinae

US-10-218-743-15

61	QY	VDPDYQDDNHNHNSWEKRGVERFNNILKKNPELITMTISLGWYEGSEKYSQMAANPTTYRQOF	120
80	DB	VDPDYQDDNHNHNSWEKRGVERFNNILKKNPELITMTISLGWYEGSEKYSQMAANPTTYRQOF	139
121	QY	IQSVLDFLOEYKFDGLDLDWEYPGSRGLGNPKDKQNYLALVRELKDAFEPHGYLLTAAVS	180
140	DB	IQSVLDFLOEYKFDGLDLDWEYPGSRGLGNPKDKQNYLALVRELKDAFEPHGYLLTAAVS	199
181	QY	PGKDKIDRAYDIKELNKLFDWNNVMTYDYHGGWENFYGHNAPLYKRPDETDELHTYFNVN	240
200	DB	PGKDKIDRAYDIKELNKLFDWNNVMTYDYHGGWENFYGHNAPLYKRPDETDELHTYFNVN	259
241	QY	YTMHYIYLNNGATRDKLVMGVPPFYGRAWSIEDRSKLGDPAPAKMSPPGFISGEEGVLSYI	300
260	DB	YTMHYIYLNNGATRDKLVMGVPPFYGRAWSIEDRSKLGDPAPAKMSPPGFISGEEGVLSYI	319
301	QY	ELCQLFQKEEWIIOYDEYYNAPYGYNDKIWVGVDLLASISCKLAFLKELGVSGVMVMSLE	360
320	DB	ELCQLFQKEEWIIOYDEYYNAPYGYNDKIWVGVDLLASISCKLAFLKELGVSGVMVMSLE	379
361	QY	NDDFKHGCHGPKPPLLKNKVNMMINGDEKNSFECILGSPSTTPTTPTTPTTPTTPTTPTTPT	420
380	DB	NDDFKHGCHGPKPPLLKNKVNMMINGDEKNSFECILGSPSTTPTTPTTPTTPTTPTTPTTPT	439
421	QY	TPPTTSPSTPTTPTTSPSTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTT	480
440	DB	TPPTTSPSTPTTPTTSPSTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTT	499
481	QY	VDGHLIKCYKEGDIPHTPTNIHKVLVCFVNGVGMVWVHIMPCPGTINCOEKLTCIGE	536
500	DB	VDGHLIKCYKEGDIPHTPTNIHKVLVCFVNGVGMVWVHIMPCPGTINCOEKLTCIGE	555

RESULT 3
 US-10-218-743-18
 ; Sequence 18; Application US/10218743
 ; Publication No. US20030096779A1
 ; GENERAL INFORMATION:
 ; APPLICANT: McCall, Catherine A.
 ; APPLICANT: Hunter, Shirley Wu
 ; APPLICANT: Weber, Eric R.
 ; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
 ; TITLE OF INVENTION: AND USES THEREOF
 ; FILE REFERENCE: AL-2-C3
 ; CURRENT APPLICATION NUMBER: US/10/218,743
 ; CURRENT FILING DATE: 2002-08-13
 ; PRIOR APPLICATION NUMBER: US/09/292,225
 ; PRIOR FILING DATE: 1999-04-15
 ; PRIOR APPLICATION NUMBER: 60/098,909
 ; PRIOR FILING DATE: 1998-09-02
 ; PRIOR APPLICATION NUMBER: 60/085,295
 ; PRIOR FILING DATE: 1998-05-13
 ; PRIOR APPLICATION NUMBER: 60/098,565
 ; PRIOR FILING DATE: 1998-04-17
 ; PRIOR APPLICATION NUMBER: 09/062,013
 ; PRIOR FILING DATE: 1998-04-17
 ; NUMBER OF SEQ ID NOS: 49
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 18
 ; LENGTH: 555
 ; TYPE: PRN
 ; ORGANISM: Dermatophagoides farinae
 US-10-218-743-18

Query Match	100.0%;	Score	3014;	DB	14;	Length	555;
Best Local Similarity	100.0%;	Frid. No.	1.3e-212;				
Matches	536;	Conservative	0;	Mismatches	0;	Indels	0;
						Gaps	0;

Qy	1	SIKEDHNDY	SKNP	MR	IV	CV	YGT	SV	HK	VP	YTT	IED	DP	FK	TH	LM	GV	FA	KID	EV	YTI	Q	60
Db	20	SIKEDHNDY	SKNP	MR	IV	CV	YGT	SV	HK	VP	YTT	IED	DP	FK	TH	LM	GV	FA	KID	EV	YTI	Q	79
Qy	61	VFDPEYQD	NHNS	WE	KRG	YER	FN	RL	RK	N	PE	LT	MI	SL	GG	YEG	SE	K	SD	MA	N	PY	120

Db 80 VFDPYQDDNHNWSEKGYERFNNLRKLNPELTTMISLGGWYEGSEKYSDMAANPTYRQOF 139
Qy 121 IOSVLDFOLEYKFDGLDLDWEYFGSRLGNPKIDKQNYLALVRELKDAEPHGYLLTAAYS 180
Db 140 IOSVLDFOLEYKFDGLDLDWEYFGSRLGNPKIDKQNYLALVRELKDAEPHGYLLTAAYS 199
Qy 181 PGKDKIDRAYDIKELNKLFDMMNMTYDYHGGWENFYGHNAPLYKRPDTEDELHTYFNNY 240
Db 200 PGKDKIDRAYDIKELNKLFDMMNMTYDYHGGWENFYGHNAPLYKRPDTEDELHTYFNNY 259
Qy 241 YTHYYLNGATRDKLVMGVPPFYGRAWSIEDRSKVLGDPAGKMSPPGFISEEGVLSYI 300
Db 260 YTHYYLNGATRDKLVMGVPPFYGRAWSIEDRSKVLGDPAGKMSPPGFISEEGVLSYI 319
Qy 301 ELQOLFQKEBWHIOYDEYNAPYGYNDKIWVGDDDLASISCKLAFKELGVSGVMWSLE 360
Db 320 ELQOLFQKEBWHIOYDEYNAPYGYNDKIWVGDDDLASISCKLAFKELGVSGVMWSLE 379
Qy 361 NDDPKGHCOPKPNLLNKNVNMINGDEKNSFECILGSPSTTTPTTPTTPTTPTTPTTPT 420
Db 380 NDDPKGHCOPKPNLLNKNVNMINGDEKNSFECILGSPSTTTPTTPTTPTTPTTPTTPT 439
Qy 421 TPT 480
Db 440 TPT 499
Qy 481 VDGLIKCYKEGDIHPHTNIHKYLVCFFVNGGWWHIMCPPGTIWCQEKLCIG 536
Db 500 VDGLIKCYKEGDIHPHTNIHKYLVCFFVNGGWWHIMCPPGTIWCQEKLCIG 555

RESULT 4
US-10-218-743-41
; Sequence 41, Application US/10218743
; Publication No. US20030096779A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/10/218,743
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/09/292,225
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: 60/098,909
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/085,295
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/098,565
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: 09/062,013
; PRIOR FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 41
; LENGTH: 490
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-10-218-743-41

Query Match 82.1%; Score 2475; DB 14; Length 490;
Best Local Similarity 82.5%; Pred. No. 3.6e-173;
Matches 443; Conservative 21; Mismatches 21; Indels 52; Gaps 2;
Qy 3 KRDNHNSKPMRIVCYVGTWSVYHKVDPTIEDIDPFKCTHLMYGFADKIDYKTIQVF 62
Db 3 KRDNHNSKPMRIVCYVGTWSVYHKVDPTIEDIDPFKCTHLMYGFADKIDYKTIQVF 62
Qy 63 DPYQDDNHNWSEKGYERFNNLRKLNPELTTMISLGGWYEGSEKYSDMAANPTYRQOF 122

Db 63 DPFODDNHNWSEKGYERFNNLRKLNPELTTMISLGGWYEGSEKYSDMAANPTYRQOF 122
Qy 123 SVLDFOLEYKFDGLDLDWEYFGSRLGNPKIDKQNYLALVRELKDAEPHGYLLTAAYS 182
Db 123 SVLDFOLEYKFDGLDLDWEYFGSRLGNPKIDKQNYLALVRELKDAEPHGYLLTAAYS 182
Qy 183 KDKIDRAYDIKELNKLFDMMNMTYDYHGGWENFYGHNAPLYKRPDTEDELHTYFNNY 242
Db 183 KDKIDRAYDIKELNKLFDMMNMTYDYHGGWENFYGHNAPLYKRPDTEDELHTYFNNY 242
Qy 243 MYHYLNGATRDKLVMGVPPFYGRAWSIEDRSKVLGDPAGKMSPPGFISEEGVLSYI 302
Db 243 MYHYLNGATRDKLVMGVPPFYGRAWSIEDRSKVLGDPAGKMSPPGFISEEGVLSYI 302
Qy 303 COLFQKEBWHIOYDEYNAPYGYNDKIWVGDDDLASISCKLAFKELGVSGVMWSLE 362
Db 303 COLFQKEBWHIOYDEYNAPYGYNDKIWVGDDDLASISCKLAFKELGVSGVMWSLE 362
Qy 363 DFKGHCOPKPNLLNKNVNMINGDEKNSFECILGSPSTTTPTTPTTPTTPTTPTTPTTPT 422
Db 363 DFKGHCOPKPNLLNKNVNMINGDEKNSFECILGSPSTTTPTTPTTPTTPTTPTTPTTPT 415
Qy 423 TPT 482
Db 416 TPT 433
Qy 483 GHLIKCYKEGDIHPHTNIHKYLVCFFVNGGWWHIMCPPGTIWCQEKLCIG 536
Db 434 GHLIKCYKEGDIHPHTNIHKYLVCFFVNGGWWHIMCPPGTIWCQEKLCIG 490

RESULT 5
US-10-218-743-35
; Sequence 35, Application US/10218743
; Publication No. US20030096779A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/10/218,743
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/09/292,225
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: 60/098,909
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/085,295
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/098,565
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: 09/062,013
; PRIOR FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 35
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-10-218-743-35

Query Match 82.1%; Score 2475; DB 14; Length 509;
Best Local Similarity 82.5%; Pred. No. 3.8e-173;
Matches 443; Conservative 21; Mismatches 21; Indels 52; Gaps 2;
Qy 3 KRDNHNSKPMRIVCYVGTWSVYHKVDPTIEDIDPFKCTHLMYGFADKIDYKTIQVF 62
Db 22 KRDNHNSKPMRIVCYVGTWSVYHKVDPTIEDIDPFKCTHLMYGFADKIDYKTIQVF 81
Qy 63 DPYQDDNHNWSEKGYERFNNLRKLNPELTTMISLGGWYEGSEKYSDMAANPTYRQOF 122
Db 82 DPFODDNHNWSEKGYERFNNLRKLNPELTTMISLGGWYEGSEKYSDMAANPTYRQOF 141

QY 123 SVLDFLOEYKFDGLDLDWEYFSGRLGNPKIDKQNYLALVRELKDAFEPHGYLLTAASPG 182
DB 142 SVLDFLOEYKFDGLDLDWEYFSGRLGNPKIDKQNYLALVRELKDAFEPHGYLLTAASPG 201
QY 183 KDKIDRAYDIKELNKLFDWMNVMTYDYGWENFYGHNAPLYKRPDETDELHTYFNVNYT 242
DB 202 KDKIDVAYELKELNQLFDWMNVMTYDYGWENFYGHNAPLYKRPDETDELHTYFNVNYT 261
QY 243 MHYILNNGATRDKLVMGVFFYGRAWSIEDRSKVLGDPKAGMSPPGFISGEGVLSYIEL 302
DB 262 MHYILNNGATRDKLVMGVFFYGRAWSIEDRSKVLGDPKAGMSPPGFISGEGVLSYIEL 321
QY 303 COLFOKEEWHIOYDEYNAPYGVNDKIWGVYDDLASISCKLAFLKELGELGVGMVMSLEND 362
DB 322 COLFOKEEWHIOYDEYNAPYGVNDKIWGVYDDLASISCKLAFLKELGELGVGMVMSLEND 381
QY 363 DFKHCGKPNLLKNVHNMINGDEKNSPECILGSPSTTTPTTTPTTTPTTTPTTPTTPTT 422
DB 382 DFKHCGKPNLLKNVHNMINGDEKNSPECILGSPSTTTPTTTPTTTPTTTPTTPTTPTT 434
QY 423 TTTTPTTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTT 482
DB 435 TTTTPTTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTT 452
QY 483 GHLIKYKQGYLPHPTDVKYLVCEYIATPNGGWWHIMDCPKGTRWHATLKNKCIQE 536
DB 453 GHLIKYKQGYLPHPTDVKYLVCEYIATPNGGWWHIMDCPKGTRWHATLKNKCIQE 509

RESULT 6

US-10-218-743-38
; Sequence 38, Application US/10218743
; Publication No. US20030096779A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Huxter, Shirley W.
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/10/218,743
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/09/292,225
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: 60/098,909
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/085,295
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/098,565
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: 09/062,013
; PRIOR FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 38
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-10-218-743-38

Query Match 82.1%; Score 2475; DB 14; Length 509;
Best Local Similarity 82.5%; Pred. No. 3.8e-173;
Matches 443; Conservative 21; Mismatches 21; Indels 52; Gaps 2;
QY 3 KRDNHNSKPNRIVCYVGTWSVYHKVDPTIEDIPFKCTHLMYGFADIKYKTIQVF 62
DB 22 KRDNHNSKPNRIVCYVGTWSVYHKVDPTIEDIPFKCTHLMYGFADIKYKTIQVF 81
QY 63 DPYQDDNHNSEKGYERFNNLRKNPELTMTISLGGWYEGSEKYSMAANPTVTRQFQI 122
DB 82 DPYQDDNHNSEKGYERFNNLRKNPELTMTISLGGWYEGSEKYSMAANPTVTRQFQV 141

QY 123 SVLDFLOEYKFDGLDLDWEYFSGRLGNPKIDKQNYLALVRELKDAFEPHGYLLTAASPG 182
DB 142 SVLDFLOEYKFDGLDLDWEYFSGRLGNPKIDKQNYLALVRELKDAFEPHGYLLTAASPG 201
QY 183 KDKIDRAYDIKELNKLFDWMNVMTYDYGWENFYGHNAPLYKRPDETDELHTYFNVNYT 242
DB 202 KDKIDVAYELKELNQLFDWMNVMTYDYGWENFYGHNAPLYKRPDETDELHTYFNVNYT 261
QY 243 MHYILNNGATRDKLVMGVFFYGRAWSIEDRSKVLGDPKAGMSPPGFISGEGVLSYIEL 302
DB 262 MHYILNNGATRDKLVMGVFFYGRAWSIEDRSKVLGDPKAGMSPPGFISGEGVLSYIEL 321
QY 303 COLFOKEEWHIOYDEYNAPYGVNDKIWGVYDDLASISCKLAFLKELGELGVGMVMSLEND 362
DB 322 COLFOKEEWHIOYDEYNAPYGVNDKIWGVYDDLASISCKLAFLKELGELGVGMVMSLEND 381
QY 363 DFKHCGKPNLLKNVHNMINGDEKNSPECILGSPSTTTPTTTPTTTPTTTPTTPTTPTT 422
DB 382 DFKHCGKPNLLKNVHNMINGDEKNSPECILGSPSTTTPTTTPTTTPTTTPTTPTTPTT 434
QY 423 TTTTPTTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTT 482
DB 435 TTTTPTTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTT 452
QY 483 GHLIKYKQGYLPHPTDVKYLVCEYIATPNGGWWHIMDCPKGTRWHATLKNKCIQE 536
DB 453 GHLIKYKQGYLPHPTDVKYLVCEYIATPNGGWWHIMDCPKGTRWHATLKNKCIQE 509

RESULT 7

US-10-004-219B-10
; Sequence 10, Application US/10004219B
; Publication No. US20030087414A1
; GENERAL INFORMATION:
; APPLICANT: Macroscope
; APPLICANT: Aerts, Johannes M.F.G.
; APPLICANT: Boot, Rolf G.
; TITLE OF INVENTION: A mammalian mucinase, its recombinant production, and
; TITLE OF INVENTION: its use in therapy or prophylaxis against diseases in
; TITLE OF INVENTION: which mucus is involved or infection diseases
; FILE REFERENCE: 2183-5136US
; CURRENT APPLICATION NUMBER: US/10/004,219B
; CURRENT FILING DATE: 2001-11-02
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 10
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1) (445)
; OTHER INFORMATION: /note="Human chitotriosidase"
US-10-004-219B-10

Query Match 24.5%; Score 738; DB 14; Length 445;
Best Local Similarity 34.2%; Pred. No. 7.9e-46;
Matches 152; Conservative 85; Mismatches 150; Indels 58; Gaps 11;
QY 15 RIVCYVGTWSVYHKVDPTIEDIPFKCTHLMYGFADIKYKTIQVDPYQDDNHNNSW 73
DB 2 KLVCFYTNNAQYRQGEARELPKDLPSLCTHLIYAFAGMTNHLST-----TGW 50
QY 74 -EKRGYERFNNLRKNPELTMTISLGGWYEGSEKYSMAANPTVTRQFQIQLQYK 132
DB 51 NDELTQYENGLKKNPKLTLAIGWNGFGQKTDVATANNQTFVNSAIRPLRKY 110
QY 133 FQGLDLDWEYFSGRLGNPKIDKQNYLALVRELKDAFEPHGYLLTAASPGDK 185
DB 111 FQGLDLDWEYFSGRLGNPKIDKQNYLALVRELKDAFEPHGYLLTAASPGDK 169
QY 186 IDRAYDIKELNKLFDWMNVMTYDYGWENFYGHNAPLYKRPDETDELHTYFNVNYT 245

Db 170 VDAGYEVDKIAQNLDVNLMAIDPHGSWEKVTGHNSPLYKQESGAAAS-LNVDAAVQ 228
Qy 246 YLNGATRDKLVMPVPGYGRAWSIEDRSKLGDPKAGMSPPGFISGEEGVLSYIELCQL 305
Db 229 WLQKGTTPASKLILGMPTYGRSFTLASSSDTRVGAPATGSGTPGFTKEGGLMAYEVCWS 288
Qy 306 FQKEEWHIOYDEYNAFYNDKIWGYDDLASISCKLAFKELGVSGVMVWLSLNDDEK 365
Db 289 KGATKQRIQ-DQ--KVPIFRDNQWGFDDVESFKTKVSYLKQKGLGAMVWALDLDFA 345
Qy 366 GHCQPKNPLLNKVNHNMGDEKNSFECILGPGSTTTPTPTPTPTPTPTPTPTPTPT 425
Db 346 G-----FSCNQ-----RYPLIQTLRQELSPLPLPGT 373
Qy 426 PSPT 450
Db 374 PELEVP-KPGQSPSEPHGSPGQDT 397

RESULT 8
US-10-161-547-2
; Sequence 2, Application US/10161547
; Publication No. US20030143216A1
; GENERAL INFORMATION:
; APPLICANT: Gray, Patrick W.
; APPLICANT: Tjoelker, Larry W.
; TITLE OF INVENTION: CHITINASE CHITIN-BINDING FRAGMENTS
; FILE REFERENCE: 27866/35407
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US/09/267,574
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/039,198
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-03-12
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 466
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-161-547-2

Query Match 24.5%; Score 738; DB 14; Length 466;
Best Local Similarity 34.2%; Pred. No. 8.3e-46;
Matches 152; Conservative 85; Mismatches 150; Indels 58; Gaps 11;

Qy 15 RIVCYGTWSVYHKVDP-YTIEDIDPFKCTHLMYGFAKIDEYKTIQVDFPYQDDNHSW 73
Db 23 KLVCFYTNWAQYRQGEARFLPKOLDPSLCTHLIYAFAGTNNHQLST-----TEW 71
Qy 74 -EKGYERFNNLRKNPELTMTISLGGWYEGSEKYSDMAANPTYRQFIQSVDLFLQYK 132
Db 72 NDETLYOEFNGLKKNPKLTLAIGWNFTQKFTDMVATANNRQTFVNSAIRLKYYS 131
Qy 133 FDGLDLWEYPGSRILGNPKIDKONYALVRELKDAFPHG-----YLLTAASPGKDK 185
Db 132 FDGLDLWEYPGSQ--GSPAVDKERFTTLVQDLANAFQOEAOQSGKERLLLSAAVPAGQY 190
Qy 186 IDRAYDIKELNKLFDWNVMTYDYGWENFYGHNAPLYKRPDETDDELHTYFNVTMTHY 245
Db 191 VDAGYEVDKIAQNLDVNLMAIDPHGSWEKVTGHNSPLYKQESGAAAS-LNVDAAVQ 249
Qy 246 YLNGATRDKLVMPVPGYGRAWSIEDRSKLGDPKAGMSPPGFISGEEGVLSYIELCQL 305
Db 250 WLQKGTTPASKLILGMPTYGRSFTLASSSDTRVGAPATGSGTPGFTKEGGLMAYEVCWS 309
Qy 306 FQKEEWHIOYDEYNAFYNDKIWGYDDLASISCKLAFKELGVSGVMVWLSLNDDEK 365
Db 310 KGATKQRIQ-DQ--KVPIFRDNQWGFDDVESFKTKVSYLKQKGLGAMVWALDLDFA 366
Qy 366 GHCQPKNPLLNKVNHNMGDEKNSFECILGPGSTTTPTPTPTPTPTPTPTPTPTPT 425
Db 367 G-----FSCNQ-----RYPLIQTLRQELSPLPLPGT 394

Qy 426 PSPT 450
Db 395 PELEVP-KPGQSPSEPHGSPGQDT 418

RESULT 9
US-10-161-547-4
; Sequence 4, Application US/10161547
; Publication No. US20030143216A1
; GENERAL INFORMATION:
; APPLICANT: Gray, Patrick W.
; APPLICANT: Tjoelker, Larry W.
; TITLE OF INVENTION: CHITINASE CHITIN-BINDING FRAGMENTS
; FILE REFERENCE: 27866/35407
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US/09/267,574
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/039,198
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-03-12
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 466
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-161-547-4

Query Match 24.3%; Score 732; DB 14; Length 466;
Best Local Similarity 33.9%; Pred. No. 2.3e-45;
Matches 151; Conservative 85; Mismatches 151; Indels 58; Gaps 11;

Qy 15 RIVCYGTWSVYHKVDP-YTIEDIDPFKCTHLMYGFAKIDEYKTIQVDFPYQDDNHSW 73
Db 23 KLVCFYTNWAQYRQGEARFLPKOLDPSLCTHLIYAFAGTNNHQLST-----TEW 71
Qy 74 -EKGYERFNNLRKNPELTMTISLGGWYEGSEKYSDMAANPTYRQFIQSVDLFLQYK 132
Db 72 NDETLYOEFNGLKKNPKLTLAIGWNFTQKFTDMVATANNRQTFVNSAIRLKYYS 131
Qy 133 FDGLDLWEYPGSRILGNPKIDKONYALVRELKDAFPHG-----YLLTAASPGKDK 185
Db 132 FDGLDLWEYPGSQ--GSPAVDKERFTTLVQDLANAFQOEAOQSGKERLLLSAAVPAGQY 190
Qy 186 IDRAYDIKELNKLFDWNVMTYDYGWENFYGHNAPLYKRPDETDDELHTYFNVTMTHY 245
Db 191 VDAGYEVDKIAQNLDVNLMAIDPHGSWEKVTGHNSPLYKQESGAAAS-LNVDAAVQ 249
Qy 246 YLNGATRDKLVMPVPGYGRAWSIEDRSKLGDPKAGMSPPGFISGEEGVLSYIELCQL 305
Db 250 WLQKGTTPASKLILGMPTYGRSFTLASSSDTRVGAPATGSGTPGFTKEGGLMAYEVCWS 309
Qy 306 FQKEEWHIOYDEYNAFYNDKIWGYDDLASISCKLAFKELGVSGVMVWLSLNDDEK 365
Db 310 KGATKQRIQ-DQ--KVPIFRDNQWGFDDVESFKTKVSYLKQKGLGAMVWALDLDFA 366
Qy 366 GHCQPKNPLLNKVNHNMGDEKNSFECILGPGSTTTPTPTPTPTPTPTPTPTPTPT 425
Db 367 G-----FSCNQ-----RYPLIQTLRQELSPLPLPGT 394

Qy 426 PSPT 450
Db 395 PELEVP-KPGQSPSEPHGSPGQDT 418

RESULT 10
US-10-004-219B-9
; Sequence 9, Application US/10004219B
; Publication No. US2003008741A1
; GENERAL INFORMATION:
; APPLICANT: Macrozyme
; APPLICANT: Aeris, Johannes M.F.G.

APPLICANT: Boot, Rolf G.
TITLE OF INVENTION: A mammalian mucinase, its recombinant production, and its use in therapy or prophylaxis against diseases in mammals
TITLE OF INVENTION: its use in therapy or prophylaxis against diseases in mammals
TITLE OF INVENTION: which mucus is involved or infection diseases
FILE REFERENCE: 2183-5136US
CURRENT APPLICATION NUMBER: US/10/004,219B
CURRENT FILING DATE: 2001-11-02
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patent in Ver. 2.1
SEQ ID NO 9
LENGTH: 452
TYPE: PRT
ORGANISM: Mus musculus
FEATURE: SITE
NAME/KEY: (1)..(452)
LOCATION: (1)..(452)
OTHER INFORMATION: /note="Mouse AMCase"
US-10-004-219B-9

Query Match 24.2%; Score 729.5; DB 14; Length 452;
Best Local Similarity 37.0%; Pred. No. 3.4e-45;
Matches 154; Conservative 69; Mismatches 144; Indels 49; Gaps 11;

QY 16 IVCYGTWSVYHK-VDPTTIEDIDPFKCTHLMYGFADKIDYKTIQVDPYQDDNHNW- 73
DB 3 LICFTNWAQYRPGLSGSKPDDINPCLCTHLYAFAGQNNNEITT-----IEWN 51
QY 74 EKRGYERFNNLRKNPELTMTISLGVYEGSEKYSMDMAANPTYRQOFIQSVLDFLOEYKF 133
DB 52 DVTLYKAENLKNRNSKULTLAIGWNFGTAPPTTVMSTQNRQTFTTSVIFLQYGF 111
QY 134 DGLDLDWEYFPGSRGPNKIDKQNYLALVRELKDAFEPHG-----YLLTAASVPGKDKI 186
DB 112 DGLDLDWEYFPGSR-GSPPODKHLFTVLVKENREAFQEAIESNRRLMTVAAGGINSI 170
QY 187 DRAYDIKELNKLFDMMNVTYDYGWENFYGHNAPLYKRPDETDELHTYFNNVTMYY 246
DB 171 QAGYEIPELSKYLDPIHVTYDLHGSWEYTGENSEPLYKYPTETGS-NAYLVNDVYVNYW 229
QY 247 LNNGATRDKLVMGVFFYGRANSIEDRSKLGDPAGKNSPPGFISGEGVLSYIELCOLF 306
DB 230 KNGGAPAEKLVGPEYGHFTILRNPSDNGIGAPTSGDPAGAYTRQAGFWAYYEICTFL 289
QY 307 QK---EEWHIQDEYNAPYGVNDKIWGYDDLASISCKLAFKELGSGVGMVWSLEND 363
DB 290 RSGATEVW----DASQEVPIAYKANWLGYNIKSFSVKAQWLKONFGGAMWALDLD 345
QY 364 FK-G-HCG-----PKNPLLNKVNMINNGDEKNSFCILGSPSTTTPTTTPTTTP 414
DB 346 FTGSPFCDOGKFLTSTLNKA-----LGISTEGCTAPDVPSEVTTTP 386

RESULT 11
US-10-004-219B-4
Sequence 4, Application US/10004219B
Publication No. US20030087414A1
GENERAL INFORMATION:
APPLICANT: Macrozyme
APPLICANT: Aerts, Johannes M.F.G.
APPLICANT: Boot, Rolf G.
TITLE OF INVENTION: A mammalian mucinase, its recombinant production, and its use in therapy or prophylaxis against diseases in mammals
TITLE OF INVENTION: which mucus is involved or infection diseases
FILE REFERENCE: 2183-5136US
CURRENT APPLICATION NUMBER: US/10/004,219B
CURRENT FILING DATE: 2001-11-02
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patent in Ver. 2.1
SEQ ID NO 4
LENGTH: 473
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:

APPLICANT: Boot, Rolf G.
TITLE OF INVENTION: A mammalian mucinase, its recombinant production, and its use in therapy or prophylaxis against diseases in mammals
TITLE OF INVENTION: which mucus is involved or infection diseases
FILE REFERENCE: 2183-5136US
CURRENT APPLICATION NUMBER: US/10/004,219B
CURRENT FILING DATE: 2001-11-02
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patent in Ver. 2.1
SEQ ID NO 9
LENGTH: 452
TYPE: PRT
ORGANISM: Mus musculus
FEATURE: SITE
NAME/KEY: (1)..(452)
LOCATION: (1)..(452)
OTHER INFORMATION: /note="Mouse AMCase"
US-10-004-219B-9

Query Match 24.2%; Score 729.5; DB 14; Length 452;
Best Local Similarity 37.0%; Pred. No. 3.4e-45;
Matches 154; Conservative 69; Mismatches 144; Indels 49; Gaps 11;

QY 16 IVCYGTWSVYHK-VDPTTIEDIDPFKCTHLMYGFADKIDYKTIQVDPYQDDNHNW- 73
DB 3 LICFTNWAQYRPGLSGSKPDDINPCLCTHLYAFAGQNNNEITT-----IEWN 51
QY 74 EKRGYERFNNLRKNPELTMTISLGVYEGSEKYSMDMAANPTYRQOFIQSVLDFLOEYKF 133
DB 52 DVTLYKAENLKNRNSKULTLAIGWNFGTAPPTTVMSTQNRQTFTTSVIFLQYGF 111
QY 134 DGLDLDWEYFPGSRGPNKIDKQNYLALVRELKDAFEPHG-----YLLTAASVPGKDKI 186
DB 112 DGLDLDWEYFPGSR-GSPPODKHLFTVLVKENREAFQEAIESNRRLMTVAAGGINSI 170
QY 187 DRAYDIKELNKLFDMMNVTYDYGWENFYGHNAPLYKRPDETDELHTYFNNVTMYY 246
DB 171 QAGYEIPELSKYLDPIHVTYDLHGSWEYTGENSEPLYKYPTETGS-NAYLVNDVYVNYW 229
QY 247 LNNGATRDKLVMGVFFYGRANSIEDRSKLGDPAGKNSPPGFISGEGVLSYIELCOLF 306
DB 230 KNGGAPAEKLVGPEYGHFTILRNPSDNGIGAPTSGDPAGAYTRQAGFWAYYEICTFL 289
QY 307 QK---EEWHIQDEYNAPYGVNDKIWGYDDLASISCKLAFKELGSGVGMVWSLEND 363
DB 290 RSGATEVW----DASQEVPIAYKANWLGYNIKSFSVKAQWLKONFGGAMWALDLD 345
QY 364 FK-G-HCG-----PKNPLLNKVNMINNGDEKNSFCILGSPSTTTPTTTPTTTP 414
DB 346 FTGSPFCDOGKFLTSTLNKA-----LGISTEGCTAPDVPSEVTTTP 386

RESULT 11
US-10-004-219B-4
Sequence 4, Application US/10004219B
Publication No. US20030087414A1
GENERAL INFORMATION:
APPLICANT: Macrozyme
APPLICANT: Aerts, Johannes M.F.G.
APPLICANT: Boot, Rolf G.
TITLE OF INVENTION: A mammalian mucinase, its recombinant production, and its use in therapy or prophylaxis against diseases in mammals
TITLE OF INVENTION: which mucus is involved or infection diseases
FILE REFERENCE: 2183-5136US
CURRENT APPLICATION NUMBER: US/10/004,219B
CURRENT FILING DATE: 2001-11-02
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patent in Ver. 2.1
SEQ ID NO 4
LENGTH: 473
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: mouse AMCase
OTHER INFORMATION: amino acid sequence deduced from cDNA sequence
US-10-004-219B-4

Query Match 24.2%; Score 729.5; DB 14; Length 473;
Best Local Similarity 37.0%; Pred. No. 3.6e-45;
Matches 154; Conservative 69; Mismatches 144; Indels 49; Gaps 11;

QY 16 IVCYGTWSVYHK-VDPTTIEDIDPFKCTHLMYGFADKIDYKTIQVDPYQDDNHNW- 73
DB 24 LICFTNWAQYRPGLSGSKPDDINPCLCTHLYAFAGQNNNEITT-----IEWN 72
QY 74 EKRGYERFNNLRKNPELTMTISLGVYEGSEKYSMDMAANPTYRQOFIQSVLDFLOEYKF 133
DB 73 DVTLYKAENLKNRNSKULTLAIGWNFGTAPPTTVMSTQNRQTFTTSVIFLQYGF 132
QY 134 DGLDLDWEYFPGSRGPNKIDKQNYLALVRELKDAFEPHG-----YLLTAASVPGKDKI 186
DB 133 DGLDLDWEYFPGSR-GSPPODKHLFTVLVKENREAFQEAIESNRRLMTVAAGGINSI 191
QY 187 DRAYDIKELNKLFDMMNVTYDYGWENFYGHNAPLYKRPDETDELHTYFNNVTMYY 246
DB 192 QAGYEIPELSKYLDPIHVTYDLHGSWEYTGENSEPLYKYPTETGS-NAYLVNDVYVNYW 250
QY 247 LNNGATRDKLVMGVFFYGRANSIEDRSKLGDPAGKNSPPGFISGEGVLSYIELCOLF 306
DB 251 KNGGAPAEKLVGPEYGHFTILRNPSDNGIGAPTSGDPAGAYTRQAGFWAYYEICTFL 310
QY 307 QK---EEWHIQDEYNAPYGVNDKIWGYDDLASISCKLAFKELGSGVGMVWSLEND 363
DB 311 RSGATEVW----DASQEVPIAYKANWLGYNIKSFSVKAQWLKONFGGAMWALDLD 366
QY 364 FK-G-HCG-----PKNPLLNKVNMINNGDEKNSFCILGSPSTTTPTTTPTTTP 414
DB 367 FTGSPFCDOGKFLTSTLNKA-----LGISTEGCTAPDVPSEVTTTP 407

RESULT 12
US-10-161-547-14
Sequence 14, Application US/10161547
Publication No. US20030143216A1
GENERAL INFORMATION:
APPLICANT: Gray, Patrick W.
APPLICANT: Tjoelker, Larry W.
TITLE OF INVENTION: CHITINASE CHITIN-BINDING FRAGMENTS
FILE REFERENCE: 27866/35407
CURRENT APPLICATION NUMBER: US/10/161,547
PRIOR FILING DATE: 2002-06-03
PRIOR APPLICATION NUMBER: US/09/267,574
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/039,198
PRIOR FILING DATE: EARLIER FILING DATE: 1998-03-12
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patent in Ver. 2.0
SEQ ID NO 14
LENGTH: 373
TYPE: PRT
ORGANISM: Homo sapiens
US-10-161-547-14

Query Match 23.9%; Score 721.5; DB 14; Length 373;
Best Local Similarity 37.7%; Pred. No. 1e-44;
Matches 136; Conservative 83; Mismatches 117; Indels 25; Gaps 8;

QY 15 RIVCYGTWSVYHKVDP-YTIEDIDPFKCTHLMYGFADKIDYKTIQVDPYQDDNHNW 73
DB 2 KLVCFYTNWAQYRQGEARFLPKDLPCLCTHLYAFAGMTNHQIST-----TEW 50
QY 74 -EKRGYERFNNLRKNPELTMTISLGVYEGSEKYSMDMAANPTYRQOFIQSVLDFLOEYK 132
DB 51 NDETLYQEEFNGKLNKPKLKTLLAIGWNFGTQKFTDVTATANNRQTFTVNSAIRFLKYS 110
QY 133 FDGLDLDWEYFPGSRGPNKIDKQNYLALVRELKDAFEPHG-----YLLTAASVPGKDK 185

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Db 111 FDGLDLDWEYFGSQ--GSPAVDKERFTTLVQDLANAFQOEQAQSGKERLLLSAAVPAGQTY 169
QY 186 IDRAYDIKELNKLFDWNNVNTYDYGWENFYGHNAFLYKRPDETDELHYTFNNVTMHY 245
Db 170 VDAGEYVDKIAQNLDNFVNLWAYDPHGSWEKVTGHNSELYKQESGAAS--LNVDAAVQ 228
QY 246 YLNGATRDKLVMGVPYGRAWSIEDRSKLGDPAPKGMSPPGFISGEEGVLVIELCOL 305
Db 229 WLQKGTASKLILGMPTYGHSFTLIASSSDTRVGAPATGSGTPGFTFKEGMLAYEVCWS 288
QY 306 FQKEEMHIOYDEYNAPYGYNDKIWGYDDLASICKLAFKELGVLGVGMVWLSLENDPFK 365
Db 289 KGATKQRIQ--DQ--KVPIYIFRDNQWGFDDVESFKTKVSYLKQKGLGGMVWALDLDFA 345
QY 366 G 366
Db 346 G 346

RESULT 13
US-10-161-547-15
; Sequence 15, Application US/10161547
; Publication No. US20030143216A1
; GENERAL INFORMATION:
; APPLICANT: Gray, Patrick W.
; APPLICANT: Tjoelker, Larry W.
; TITLE OF INVENTION: CHITINASE CHITIN-BINDING FRAGMENTS
; FILE REFERENCE: 27866/35407
; CURRENT APPLICATION NUMBER: US/10/161,547
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US/09/267,574
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/039,198
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-03-12
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 15
; LENGTH: 373
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-161-547-15

Query Match 23.9%; Score 721.5; DB 14; Length 373;
Best Local Similarity 37.7%; Pred. No. 1e-44;
Matches 136; Conservative 83; Mismatches 117; Indels 25; Gaps 8;

QY 15 RIVCYVGTWSVYHKVP--YIIEDIDPKCTHLMYGFAKIDYKYTIQVDFPYQDDNHSW 73
Db 2 KLVCFYTNWACYRQGEARFLPKDLDPSLCTHLIYAFAGMTNHLST-----TEW 50
QY 74 -EKGYERENLRLKNPELTMTISLGGWYEGSEKYSMDAANPTYRQFIQSVDLFLQYK 132
Db 51 NDETLYOEFFNGLKKNPKLTLLAIGWNGFTQKFTDMVATANNROTFTVNSAIRFLRKYS 110
QY 133 FDGLDLDWEYFGSRLGNPKDKONYLALVRELKDAPEFHG-----YLLTAASVPGKDK 185
Db 111 FDGLDLDWEYFGSQ--GSPAVDKERFTTLVQDLANAFQOEQAQSGKERLLLSAAVPAGQTY 169
QY 186 IDRAYDIKELNKLFDWNNVNTYDYGWENFYGHNAFLYKRPDETDELHYTFNNVTMHY 245
Db 170 VDAGEYVDKIAQNLDNFVNLWAYDPHGSWEKVTGHNSELYKQESGAAS--LNVDAAVQ 228
QY 246 YLNGATRDKLVMGVPYGRAWSIEDRSKLGDPAPKGMSPPGFISGEEGVLVIELCOL 305
Db 229 WLQKGTASKLILGMPTYGHSFTLIASSSDTRVGAPATGSGTPGFTFKEGMLAYEVCWS 288
QY 306 FQKEEMHIOYDEYNAPYGYNDKIWGYDDLASICKLAFKELGVLGVGMVWLSLENDPFK 365
Db 289 KGATKQRIQ--DQ--KVPIYIFRDNQWGFDDVESFKTKVSYLKQKGLGGMVWALDLDFA 345
QY 366 G 366
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Db 346 G 346

RESULT 14
US-10-004-219B-14
; Sequence 14, Application US/10004219B
; Publication No. US20030087414A1
; GENERAL INFORMATION:
; APPLICANT: Aerts, Johannes M.F.G.
; APPLICANT: Boot, Rolf G.
; TITLE OF INVENTION: A mammalian mucinase, its recombinant production, and
; TITLE OF INVENTION: its use in therapy or prophylaxis against diseases in
; TITLE OF INVENTION: which mucus is involved or infection diseases
; FILE REFERENCE: 2183-5136US
; CURRENT APPLICATION NUMBER: US/10/004,219B
; CURRENT FILING DATE: 2001-11-02
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 14
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(455)
; OTHER INFORMATION: /note="Human AMCase"
US-10-004-219B-14

Query Match 23.5%; Score 708.5; DB 14; Length 455;
Best Local Similarity 35.9%; Pred. No. 1.2e-43;
Matches 149; Conservative 75; Mismatches 154; Indels 37; Gaps 10;

QY 15 RIVCYVGTWSVYHK--VDPVTTEDIDPFKCTHLMYGFAKIDYKYTIQVDFPYQDDNHSW 73
Db 2 QLTCTFTWACYRPGLGREFMFDNIDPCLCTHLIYAFAGRONNEITT-----LEW 50
QY 74 -EKGYERENLRLKNPELTMTISLGGWYEGSEKYSMDAANPTYRQFIQSVDLFLQYK 132
Db 51 NDETLYOEFFNGLKKNPKLTLLAIGWNGFTQKFTDMVATANNROTFTVNSAIRFLRKYS 110
QY 133 FDGLDLDWEYFGSRLGNPKDKONYLALVRELKDAPEFHG-----YLLTAASVPGKDK 185
Db 111 FDGLDLDWEYFGSR--GSPPDQKHLFTVLVQEMREAFQEAQINKPRLMTAAVAAGISN 169
QY 186 IDRAYDIKELNKLFDWNNVNTYDYGWENFYGHNAFLYKRPDETDELHYTFNNVTMHY 245
Db 170 IOSGYEIPQLSOYLDYIHMVTDLHGSWEGTGENSPLYKYPTDTGS--NAVNLVDYVMKY 228
QY 246 YLNGATRDKLVMGVPYGRAWSIEDRSKLGDPAPKGMSPPGFISGEEGVLVIELCOL 305
Db 229 WKDNGAPAEKLVGFTYGHNFILSNPNTGIGFTSAGAPGVAKESGWAYVEIC-T 287
QY 306 FQKEEMHIOYDEYNAPYGYNDKIWGYDDLASICKLAFKELGVLGVGMVWLSLENDPFK 365
Db 288 FLKNGATQGDAPQEPVPYAYQGNVWVGYDNISPDIAQWLKHNKFGAMVWALDLDFT 347
QY 366 G-HCGP-KNPLKNVHNMINGDEKNSFECILGPSFTTTPTPTPTPTPTPTPTPTPTPS 418
Db 348 GTFCNQKFPPLT-----STLKKALGLQASCTAPAQPIETITAAPSGS 390

RESULT 15
US-10-004-219B-1
; Sequence 1, Application US/10004219B
; Publication No. US20030087414A1
; GENERAL INFORMATION:
; APPLICANT: Aerts, Johannes M.F.G.
; APPLICANT: Boot, Rolf G.
; TITLE OF INVENTION: A mammalian mucinase, its recombinant production, and
; TITLE OF INVENTION: its use in therapy or prophylaxis against diseases in
; TITLE OF INVENTION: which mucus is involved or infection diseases
```

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; FILE REFERENCE: 2183-5136US
; CURRENT APPLICATION NUMBER: US/10/004,219B
; CURRENT FILING DATE: 2001-11-02
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: human AMCase
; OTHER INFORMATION: amino acid sequence deduced from cDNA sequence
US-10-004-219B-1

Query Match      23.5%; Score 708.5; DB 14; Length 476;
Best Local Similarity 35.9%; Pred. No. 1.2e-43;
Matches 149; Conservative 75; Mismatches 154; Indels 37; Gaps 10;

QY 15 RIVCVGTWSTYHK-VDPYTTIEDIDPKCHLMYGFPAKIDBYKYTIQVDFPYQDDNHSW 73
Db 15 RIVCVGTWSTYHK-VDPYTTIEDIDPKCHLMYGFPAKIDBYKYTIQVDFPYQDDNHSW 73
QY 23 QLTCTFTNWAQYRFLGRLGFMFDNIDPCLCTHLIYAFAGRQNNETTT-----IEW 71
Db 23 QLTCTFTNWAQYRFLGRLGFMFDNIDPCLCTHLIYAFAGRQNNETTT-----IEW 71
QY 74 -EKRGYERFNNLRKLNPELTTMISLGGWYEGSEKYSDMAANPTVYRQOFIOSVLDLFLQYK 132
Db 74 -EKRGYERFNNLRKLNPELTTMISLGGWYEGSEKYSDMAANPTVYRQOFIOSVLDLFLQYK 132
QY 72 NDTVLYQAFNGLKKNKNSQLKTLAIGGNFTAPFTAVSTPENRQFTITSVIKFLQYE 131
Db 72 NDTVLYQAFNGLKKNKNSQLKTLAIGGNFTAPFTAVSTPENRQFTITSVIKFLQYE 131
QY 133 FDGLDLDWEYFGSRIGNPDKIDQNYLALVRELKDAFEPHG-----YLLTAAVSPGKOK 185
Db 133 FDGLDLDWEYFGSRIGNPDKIDQNYLALVRELKDAFEPHG-----YLLTAAVSPGKOK 185
QY 132 FDGLDPWEYFGSR-GSPPDKHLFTVLVQEMREAFQEAKQINKPRLMVTAAVAAGISN 190
Db 132 FDGLDPWEYFGSR-GSPPDKHLFTVLVQEMREAFQEAKQINKPRLMVTAAVAAGISN 190
QY 186 IDRAYDIKELNKLFDMMNVMTYDHHGWNENFYGHNAFLYKRPDETDLHTYFNVNYTMHY 245
Db 186 IDRAYDIKELNKLFDMMNVMTYDHHGWNENFYGHNAFLYKRPDETDLHTYFNVNYTMHY 245
QY 191 IQSGVEIPQLSQYLDYIHVMTYDLHGSWEGYTGENSEPLYKYPTDTGS-NAYLNVYVMNY 249
Db 191 IQSGVEIPQLSQYLDYIHVMTYDLHGSWEGYTGENSEPLYKYPTDTGS-NAYLNVYVMNY 249
QY 246 YLNGATRDKLVMGVPPFYGRAWSIEDRSKLGDPKAGMSPPGFISGEGVLSYIELCOL 305
Db 246 YLNGATRDKLVMGVPPFYGRAWSIEDRSKLGDPKAGMSPPGFISGEGVLSYIELCOL 305
QY 250 WKDNGAPAEKLIIVGPTTYGHNFILSNPNTGIGAPTSGAGPAGPYAKESGIWAYEYC-T 308
Db 250 WKDNGAPAEKLIIVGPTTYGHNFILSNPNTGIGAPTSGAGPAGPYAKESGIWAYEYC-T 308
QY 306 FQKEEWHIQYDEYYNAPYGVNDKIWGVYDDILASISCKLAFKLKELGVSGVMVWSLENDDFK 365
Db 306 FQKEEWHIQYDEYYNAPYGVNDKIWGVYDDILASISCKLAFKLKELGVSGVMVWSLENDDFK 365
QY 309 FLKNGATOGWDAPEVFPYAGVNVGVYDNTKSFDIKAQWLKHNKFGAMVWALDLDFFT 368
Db 309 FLKNGATOGWDAPEVFPYAGVNVGVYDNTKSFDIKAQWLKHNKFGAMVWALDLDFFT 368
QY 366 G-HCGP-KNPLLNKVNHNMGDEKNSPECILGPSTTTPTTTPTTTPTTTPTTPTTPTT 418
Db 366 G-HCGP-KNPLLNKVNHNMGDEKNSPECILGPSTTTPTTTPTTTPTTTPTTPTTPTT 418
QY 369 GTFCNQKFLPI-----STLKKALGLQSASCTAPAPQPIEPITRAPSGS 411
Db 369 GTFCNQKFLPI-----STLKKALGLQSASCTAPAPQPIEPITRAPSGS 411

Search completed: March 22, 2004, 07:45:53
Job time : 110.643 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 22, 2004, 06:30:23 ; Search time 162.975 Seconds
(without alignments)
929.256 Million cell updates/sec

Title: US-09-662-293-21

Perfect score: 3014

Sequence: 1 SIKEDHNDYKNPNRIYCV.....IMPCPPTIWQEKLTIGE 536

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_29Jan04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3014	100.0	536	3 AAY52525	Aay52525 House dus
2	3014	100.0	536	5 AAU96329	Aau96329 Der HW-m
3	3014	100.0	555	3 AAY52523	Aay52523 House dus
4	3014	100.0	555	5 AAU96327	Aau96327 Der HW-m
5	3014	100.0	555	5 AAU96328	Aau96328 Der HW-m
6	2475	82.1	490	3 AAY52535	Aay52535 D. pteron
7	2475	82.1	490	5 AAU96339	Aau96339 Der HW-m
8	2475	82.1	509	3 AAY52533	Aay52533 D. pteron
9	2475	82.1	509	5 AAU96337	Aau96337 Der HW-m
10	2475	82.1	509	5 AAU96338	Aau96338 Der HW-m
11	1007	33.4	525	6 ABP72636	Abp72636 Anopheles
12	848.5	28.2	4498	4 ABB58595	Abb58595 Drosophil
13	837.5	27.8	467	6 ABP72634	Abp72634 Prawn chi
14	837.5	27.8	595	4 ABB71737	Abb71737 Drosophil
15	834	27.7	554	2 AAU01824	Aau01824 Manduca s
16	834	27.7	554	3 AAB07183	Aab07183 Manduca s
17	834	27.7	554	6 ABP72619	Abp72619 Manduca s
18	830.5	27.6	460	4 ABB64366	Abb64366 Drosophil
19	819	27.2	565	6 ABP72625	Abp72625 Bombyx mo
20	812.5	27.0	583	5 AAE28197	Aae28197 Flea chit
21	811.5	26.9	559	5 AAE28199	Aae28199 Flea chit
22	809.5	26.9	635	5 AAE28203	Aae28203 Flea chit
23	808	26.8	574	6 ABP72635	Abp72635 Aedes aeg
24	801.5	26.6	483	6 ABP72633	Abp72633 Chelonus
25	779.5	25.9	553	6 ABP72626	Abp72626 Hyphantri

26	738	24.5	466	2 AAW08584	Aaw08584 Human 50
27	738	24.5	466	2 AAW40259	Aaw40259 Human chi
28	738	24.5	466	2 AAY42425	Aay42425 MO-218 cl
29	738	24.5	466	4 AAE00432	Aae00432 Human chi
30	738	24.5	466	5 AAE25903	Aae25903 Human chi
31	738	24.5	466	5 ABB76291	Abb76291 Human chi
32	735.5	24.4	459	7 ADC24231	Adc24231 Human NOV
33	732.5	24.3	387	2 AAW08585	Aaw08585 Human 39
34	732	24.3	447	7 ADC24237	Adc24237 Human NOV
35	732	24.3	466	2 AAW40260	Aaw40260 Human chi
36	732	24.3	466	2 AAY42426	Aay42426 MO-13B cl
37	732	24.3	466	4 AAE300433	Aae300433 Human chi
38	732	24.3	466	5 AAE25904	Aae25904 Human chi
39	732	24.3	466	5 ABB76292	Abb76292 Human chi
40	731	24.3	466	2 AAW311498	Aaw311498 Human chi
41	729.5	24.2	452	7 ABR55544	Abr55544 Amino aci
42	729.5	24.2	473	7 ABR55543	Abr55543 Amino aci
43	729.5	24.2	520	6 ABU09914	Abu09914 Partial m
44	727.5	24.1	473	7 ADC51464	Adc51464 Chitotria
45	723	24.0	466	6 ABP72621	Abp72621 Human chi

ALIGNMENTS

RESULT 1

AAV52525

ID AAY52525 standard; protein; 536 AA.

XX AAY52525;

XX 22-FEB-2000 (first entry)

XX House dust mite (D. farinae) mite allergen protein (map) PDerf98-536.

XX Mite allergen protein; map; high molecular weight; Hmw; mapB;

XX house dust mite; IgE; immunoglobulin E; allergen; mapA; mapB;

XX hypersensitivity reaction; therapy; treatment; diagnosis; human; feline;

XX canine; veterinary; antibody; vaccine; immunisation.

XX Dermatophagoides farinae.

XX WO9554349-A2.

XX 28-OCT-1999.

XX 16-APR-1999; 99WO-US008524.

XX 17-APR-1998; 98US-00062013.

XX 13-MAY-1998; 98US-0085295P.

XX 02-SEP-1998; 98US-0098909P.

XX (HESK-) HESKA CORP.

XX McCall CA, Hunter SW, Weber ER;

XX WPI; 2000-052700/04.

XX N-PSDB; AA238579, AA238580.

XX Novel high molecular weight Dermatophagoides nucleic acid polypeptides

XX used to modify an animals' hypersensitivity to mite allergens.

XX Claim 3; Page 125-127; 154pp; English.

XX This sequence represents Dermatophagoides farinae mite allergen protein

XX (map) PDerf98-536, the mature form of PDerf98-555 (AAY52523). PDerf98-536

XX has a molecular weight of 98 kD, comprising 536 amino acids, and is a

XX component of the Dermatophagoides farinae high molecular weight mite

XX allergen protein (Hmw-map) composition. The Hmw-map composition was

XX isolated from a D. farinae homogenate by gel filtration, with each

XX fraction being analysed for the presence of proteins that bound to IgE

XX present in mite-allergic dog antisera. Mite allergenic proteins and

XX peptides, and nucleic acids encoding them, may be used in therapeutic

CC compositions to modify an animal's hypersensitivity reaction to mite
CC allergens. Animals that may be treated include mammals and birds,
CC especially felines, canines, equines, humans, other pets, and work or
CC domestic animals. The proteins or fragments may also be used to diagnose
CC allergies via a skin test. The proteins and peptides can also be used to
CC raise antibodies, which have a variety of potential uses. For example,
CC they can be used as vaccines to passively immunise animals against dust
CC mite hypersensitivity, as positive controls in test kits and as tools to
CC recover desired dust mite allergens from a mixture of proteins
XX
SQ Sequence 536 AA;

Query Match 100.0%; Score 3014; DB 3; Length 536;
Best Local Similarity 100.0%; Pred. No. 3.7e-210;
Matches 536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SIKRDNDYKSNPMRIVCVYGVTSVYHKVDPYTIEDIDPFKCTHLMYGFAKIDYKYTIQ 60
Db 1 SIKRDNDYKSNPMRIVCVYGVTSVYHKVDPYTIEDIDPFKCTHLMYGFAKIDYKYTIQ 60
Qy 61 VFDPYQDDNHNSEKRGYERFNNLRNLKNPELTMTISLGGWYEGSEKYSDMAANPTYRQOF 120
Db 61 VFDPYQDDNHNSEKRGYERFNNLRNLKNPELTMTISLGGWYEGSEKYSDMAANPTYRQOF 120
Qy 121 IQSVLDFLOEYKFDGLDWEYPSGRLGNPKDKQNYLALVRELKDAFEPHGILLTAAYS 180
Db 121 IQSVLDFLOEYKFDGLDWEYPSGRLGNPKDKQNYLALVRELKDAFEPHGILLTAAYS 180
Qy 181 PGKDKIDRAYDIKELNKLFDWMVNTYDYGHWENFYGHNAPLYKRPDETDELHTYFNVN 240
Db 181 PGKDKIDRAYDIKELNKLFDWMVNTYDYGHWENFYGHNAPLYKRPDETDELHTYFNVN 240
Qy 241 YTMHYLLNNGATRDKLVMGVPFYGRAWSIEDRSKILGDPKAGMSPPGFISGEEGLSYI 300
Db 241 YTMHYLLNNGATRDKLVMGVPFYGRAWSIEDRSKILGDPKAGMSPPGFISGEEGLSYI 300
Qy 301 ELCOLFQKEEWHIQDEYVYNAFYNDKIWGVYDDLASISCKLAFKELGVSVMVWSLE 360
Db 301 ELCOLFQKEEWHIQDEYVYNAFYNDKIWGVYDDLASISCKLAFKELGVSVMVWSLE 360
Qy 361 NDDFKHCGKPNPLLNKVNHNMGDEKNSFECILGPSTTTPTTPTTPTTPTTPTTPTTPT 420
Db 361 NDDFKHCGKPNPLLNKVNHNMGDEKNSFECILGPSTTTPTTPTTPTTPTTPTTPTTPT 420
Qy 421 TPTTPTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPT 480
Db 421 TPTTPTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPT 480
Qy 481 VDGHILIKCYKEGDIHPHTNIHKYLVCFVNGWVWHIMPCPPGTIWCOEKLTCIGE 536
Db 481 VDGHILIKCYKEGDIHPHTNIHKYLVCFVNGWVWHIMPCPPGTIWCOEKLTCIGE 536

RESULT 2
AAU96329 standard; protein; 536 AA.
ID AAU96329
XX AC AAU96329;
XX AC
XX AC
DT 15-JUL-2002 (first entry)
XX
DE Der HMW-map polypeptide #16.
XX
XX Der HMW-map; American house dust mite; antiallergic; mite; Ige;
KW mite allergenic protein; immunoglobulin E; hypersensitivity;
KW immunocomplex formation.
XX
XX Dermatophagoides farinae.
OS
XX WO200222807-A2.
XX
XX
PD 21-MAR-2002.
XX

PF 14-SEP-2001; 2001WO-US028730.
XX
PR 14-SEP-2000; 2000US-00662293.
XX
PA (HESK-) HESKA CORP.
XX
XX McCall CA, Hunter SW, Weber ER;
XX WPI; 2002-351888/38.
DR N-PSDB; ABK69575.
XX
XX New mite allergenic protein isolated from Dermatophagoides, designated
PT Der HMW-map protein, useful as a vaccine for treating mite allergy.
PT
PS Claim 12; Page 125-127; 161pp; English.
XX
CC The invention relates to an isolated mite allergenic protein of
CC Dermatophagoides, designated Der HMW-map protein, and its related nucleic
CC acid. The Der HMW-map protein is useful for eliciting an immune response
CC against Der HMW-map protein. The protein or a reagent comprising a non-
CC proteinaceous epitope is useful for identifying an animal (e.g., dog,
CC cat) susceptible to or having an allergic response to a mite. A
CC therapeutic composition is useful for desensitising a host animal to an
CC allergic response to a mite. The DNA and protein can be used in the
CC detection of anti-Der HMW-map antibodies in animal fluids, and inhibition
CC of immunoglobulin (Ig)E or Der HMW-map protein activity associated with a
CC disease. Antibodies that bind to Der HMW-map are useful for inhibiting
CC binding of proteins to IgE, to prevent immunocomplex formation, thus
CC reducing hypersensitivity responses to mite allergens, and as vaccines
CC against mite allergen hypersensitivity. Sequences AAU96314-AAU96342
CC represent Der HMW-map polypeptides of the invention
XX
SQ Sequence 536 AA;

Query Match 100.0%; Score 3014; DB 5; Length 536;
Best Local Similarity 100.0%; Pred. No. 3.7e-210;
Matches 536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SIKRDNDYKSNPMRIVCVYGVTSVYHKVDPYTIEDIDPFKCTHLMYGFAKIDYKYTIQ 60
Db 1 SIKRDNDYKSNPMRIVCVYGVTSVYHKVDPYTIEDIDPFKCTHLMYGFAKIDYKYTIQ 60
Qy 61 VFDPYQDDNHNSEKRGYERFNNLRNLKNPELTMTISLGGWYEGSEKYSDMAANPTYRQOF 120
Db 61 VFDPYQDDNHNSEKRGYERFNNLRNLKNPELTMTISLGGWYEGSEKYSDMAANPTYRQOF 120
Qy 121 IQSVLDFLOEYKFDGLDWEYPSGRLGNPKDKQNYLALVRELKDAFEPHGILLTAAYS 180
Db 121 IQSVLDFLOEYKFDGLDWEYPSGRLGNPKDKQNYLALVRELKDAFEPHGILLTAAYS 180
Qy 181 PGKDKIDRAYDIKELNKLFDWMVNTYDYGHWENFYGHNAPLYKRPDETDELHTYFNVN 240
Db 181 PGKDKIDRAYDIKELNKLFDWMVNTYDYGHWENFYGHNAPLYKRPDETDELHTYFNVN 240
Qy 241 YTMHYLLNNGATRDKLVMGVPFYGRAWSIEDRSKILGDPKAGMSPPGFISGEEGLSYI 300
Db 241 YTMHYLLNNGATRDKLVMGVPFYGRAWSIEDRSKILGDPKAGMSPPGFISGEEGLSYI 300
Qy 301 ELCOLFQKEEWHIQDEYVYNAFYNDKIWGVYDDLASISCKLAFKELGVSVMVWSLE 360
Db 301 ELCOLFQKEEWHIQDEYVYNAFYNDKIWGVYDDLASISCKLAFKELGVSVMVWSLE 360
Qy 361 NDDFKHCGKPNPLLNKVNHNMGDEKNSFECILGPSTTTPTTPTTPTTPTTPTTPTTPT 420
Db 361 NDDFKHCGKPNPLLNKVNHNMGDEKNSFECILGPSTTTPTTPTTPTTPTTPTTPTTPT 420
Qy 421 TPTTPTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPT 480
Db 421 TPTTPTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPT 480
Qy 481 VDGHILIKCYKEGDIHPHTNIHKYLVCFVNGWVWHIMPCPPGTIWCOEKLTCIGE 536
Db 481 VDGHILIKCYKEGDIHPHTNIHKYLVCFVNGWVWHIMPCPPGTIWCOEKLTCIGE 536

RESULT 3
 ID AAY52523 standard; protein; 555 AA.
 AC AAY52523;
 DT 22-FEB-2000 (first entry)
 DE House dust mite (D. farinae) mite allergen protein (map) Pderf98-555.
 KW Mite allergen protein; map; high molecular weight; Hmw-map; allergen;
 KW house dust mite; IgE; immunoglobulin E; allergen; mapA; mapB;
 KW hypersensitivity reaction; therapy; treatment; diagnosis; human; feline;
 KW canine; veterinary; antibody; vaccine; immunisation.
 OS Dermatophagoides farinae.
 PH Key Location/Qualifiers
 FT Peptide 1..19
 FT Protein /note= "Signal peptide"
 FT Protein 20..555
 FT Protein /note= "Mature Pderf98-555"
 XX W09954349-A2.
 XX 28-OCT-1999.
 XX 16-APR-1999; 99WO-US008524.
 XX 17-APR-1998; 98US-00062013.
 XX 13-MAY-1998; 98US-0085295P.
 XX 02-SEP-1998; 98US-0098909P.
 XX (HESK-) HESKA CORP.
 XX Mccall CA, Hunter SW, Weber ER;
 WPI; 2000-052700/04.
 N-PSDB; AAZ38575, AAZ38576, AAZ38577, AAZ38578.
 Novel high molecular weight Dermatophagoides nucleic acid polypeptides
 used to modify an animals' hypersensitivity to mite allergens.
 Claim 3; Page 111-113; 154pp; English.
 This sequence represents Dermatophagoides farinae mite allergen protein
 (map) Pderf98-555. Pderf98-555 has a molecular weight of 98 kD,
 comprising 555 amino acids, and is a component of the Dermatophagoides
 farinae high molecular weight mite allergen protein (Hmw-map)
 composition. The Hmw-map composition was isolated from a D. farinae
 homogenate by gel filtration, with each fraction being analysed for the
 presence of proteins that bound to IgE present in mite-allergic dog
 antisera. Mite allergenic proteins and peptides, and nucleic acids
 encoding them, may be used in therapeutic compositions to modify an
 animal's hypersensitivity reaction to mite allergens. Animals that may be
 treated include mammals and birds, especially felines, canines, equines,
 humans, other pets, and work or domestic animals. The proteins or
 fragments may also be used to diagnose allergies via a skin test. The
 proteins and peptides can also be used to raise antibodies, which have a
 variety of potential uses. For example, they can be used as vaccines to
 passively immunise animals against dust mite hypersensitivity, as
 positive controls in test kits and as tools to recover desired dust mite
 allergens from a mixture of proteins
 Sequence 555 AA;
 Query March 100.0%; Score 3014; DB 3; Length 555;
 Best Local Similarity 100.0%; Pred. No. 3.9e-210;
 Matches 536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 SIKRDNDYSKNPVRIVCVGTWSVYHKVDPTTIEDIDPFKCTHLMYGFADIKYKTIQ 60

Db 20 SIKRDNDYSKNPVRIVCVGTWSVYHKVDPTTIEDIDPFKCTHLMYGFADIKYKTIQ 79
 Qy 61 VEDPYODDNDHNSWEKRGYERFNNLELKNPELTMTLSLGGWEGSEKYSMDAANPYRQOF 120
 Db 80 VEDPYODDNDHNSWEKRGYERFNNLELKNPELTMTLSLGGWEGSEKYSMDAANPYRQOF 139
 Qy 121 IOSVLDLFLQYKFDGLDLDWEYFGSRLGNPKIDKQNYLALVRELKDAFEPHGYLLTAAVS 180
 Db 140 IOSVLDLFLQYKFDGLDLDWEYFGSRLGNPKIDKQNYLALVRELKDAFEPHGYLLTAAVS 199
 Qy 181 PGKIDIDRAYDIKELNKLFDWNNVMTYDHGWNFYGHNAPLYKRPDETDELHTYFNNV 240
 Db 200 PGKIDIDRAYDIKELNKLFDWNNVMTYDHGWNFYGHNAPLYKRPDETDELHTYFNNV 259
 Qy 241 YTHYYLNGATRDKLVMGVFPFYGRAWSIEDRSKLKLGDPAGKMSPPGFISGEEGVLSVI 300
 Db 260 YTHYYLNGATRDKLVMGVFPFYGRAWSIEDRSKLKLGDPAGKMSPPGFISGEEGVLSVI 319
 Qy 301 ELCQLFOKEEWHIQYDEYVNAFYNDKIWGYDDLASISCKLAFELKELGSGVNVWSLE 360
 Db 320 ELCQLFOKEEWHIQYDEYVNAFYNDKIWGYDDLASISCKLAFELKELGSGVNVWSLE 379
 Qy 361 NDDFKHGCGKPNLLKVNMMINGDEKNSFECLIGPSTTTPTPTPTPTPTPTPTPTPTPTPT 420
 Db 380 NDDFKHGCGKPNLLKVNMMINGDEKNSFECLIGPSTTTPTPTPTPTPTPTPTPTPTPTPT 439
 Qy 421 TPTTPT 480
 Db 440 TPTTPT 499
 Qy 481 VDGHLIKCYKEGDIPHPTNIHKYLVCEFGVNGWVHIMPCPPGTIWCQKLTICGE 536
 Db 500 VDGHLIKCYKEGDIPHPTNIHKYLVCEFGVNGWVHIMPCPPGTIWCQKLTICGE 555

RESULT 4
 AAU96327
 ID AAU96327 standard; protein; 555 AA.
 AC AAU96327;
 DT 15-JUL-2002 (first entry)
 DE Der Hmw-map polypeptide #14.
 KW Der Hmw-map; American house dust mite; antiallergic; mite; IgE;
 KW mite allergenic protein; immunoglobulin E; hypersensitivity;
 KW immunocomplex formation.
 OS Dermatophagoides farinae.
 PN W0200222807-A2.
 XX 21-MAR-2002.
 XX 14-SEP-2001; 2001WO-US028730.
 XX 14-SEP-2000; 2000US-00662293.
 XX (HESK-) HESKA CORP.
 XX Mccall CA, Hunter SW, Weber ER;
 WPI; 2002-351888/38.
 DR N-PSDB; ABK69571.
 XX New mite allergenic protein isolated from Dermatophagoides, designated
 Der Hmw-map protein, useful as a vaccine for treating mite allergy.
 Claim 12; Page 114-116; 161pp; English.
 The invention relates to an isolated mite allergenic protein of

CC Dermatophagoides, designated Der HMW-map protein, and its related nucleic
 CC acid. The Der HMW-map protein is useful for eliciting an immune response
 CC against Der HMW-map protein. The protein or a reagent comprising a non-
 CC proteinaceous epitope is useful for identifying an animal (e.g., dog,
 CC cat) susceptible to or having an allergic response to a mite. A
 CC therapeutic composition is useful for desensitising a host animal to an
 CC allergic response to a mite. The DNA and protein can be used in the
 CC detection of anti-Der HMW-map antibodies in animal fluids, and inhibition
 CC of immunoglobulin (Ig)E or Der HMW-map protein activity associated with a
 CC disease. Antibodies that bind to Der HMW-map are useful for inhibiting
 CC binding of proteins to IgE, to prevent immunocomplex formation, thus
 CC reducing hypersensitivity responses to mite allergens, and as vaccines
 CC against mite allergen hypersensitivity. Sequences AAU96314-AAU96342
 CC represent Der HMW-map polypeptides of the invention
 XX
 XX Sequence 555 AA;

Query Match 100.0%; Score 3014; DB 5; Length 555;
 Best Local Similarity 100.0%; Pred. No. 3.9e-210;
 Matches 536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIKRDNDYSKNPMRIVCVGTWVSYYHKVDPTTIEDIDPFKCTHLMYGFADIKYKTIQ 60
 Db 20 SIKRDNDYSKNPMRIVCVGTWVSYYHKVDPTTIEDIDPFKCTHLMYGFADIKYKTIQ 79
 QY 61 VFDPPQDDNHNSEKRGYERFNNLKNPELTMTISLGGWTEGSEKYSDMAANPTYRQF 120
 Db 80 VFDPPQDDNHNSEKRGYERFNNLKNPELTMTISLGGWTEGSEKYSDMAANPTYRQF 139
 QY 121 IQSVLDFLOEYKFDGLDWEYVPSRLGNPKIDKQNYLALVRELKDAFEHGYLLTAAS 180
 Db 140 IQSVLDFLOEYKFDGLDWEYVPSRLGNPKIDKQNYLALVRELKDAFEHGYLLTAAS 199
 QY 181 PGKOKIDRAYDIKELNKLFDWNNVMTYDHGGWENFYGHNAPLYKRPDTEDELHTYFNVN 240
 Db 200 PGKOKIDRAYDIKELNKLFDWNNVMTYDHGGWENFYGHNAPLYKRPDTEDELHTYFNVN 259
 QY 241 YTMHYLLNNGATRDKLVMGVPPFYGRAMSIEDRSKILKLGDPKAGMSPPGFISGEEGVL 300
 Db 260 YTMHYLLNNGATRDKLVMGVPPFYGRAMSIEDRSKILKLGDPKAGMSPPGFISGEEGVL 319
 QY 301 ELCOLFQKEEWHIQYDEYNNAPYGYNDKIWGYDDLASISCKLAFKELGVSGVMWSLE 360
 Db 320 ELCOLFQKEEWHIQYDEYNNAPYGYNDKIWGYDDLASISCKLAFKELGVSGVMWSLE 379
 QY 361 NDDFKGHCPCPNLKNVHNMINGEKNSFECILGPSTTPTTPTTPTTPTTPTTPTTPT 420
 Db 380 NDDFKGHCPCPNLKNVHNMINGEKNSFECILGPSTTPTTPTTPTTPTTPTTPTTPT 439
 QY 421 TPTTPTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPT 480
 Db 440 TPTTPTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPT 499
 QY 481 VDGHLIKCYKGDIPHPNTIHKYLVCFVNGVMWHIMPCPPGTIWCQELTICGE 536
 Db 500 VDGHLIKCYKGDIPHPNTIHKYLVCFVNGVMWHIMPCPPGTIWCQELTICGE 555

RESULT 5

AAU96328

ID AAU96328 standard; protein; 555 AA.

XX AC

XX AC

XX AC

XX 15-JUL-2002 (first entry)

XX Der HMW-map polypeptide #15.

XX DE

XX KW

XX KW

XX KW

XX OS

XX OS

XX OS

XX OS

XX OS

XX OS

XX OS

XX PN WO200222807-A2.
 XX PD 21-MAR-2002.
 XX PF 14-SEP-2001; 2001WO-US028730.
 XX PR 14-SEP-2000; 2000US-00662293.
 XX PA (HESK-) HESKA CORP.
 XX PI McCall CA, Hunter SW, Weber ER;
 XX DR WPI; 2002-351888/38.
 XX DR N-PSDB; ABK69573.
 XX PT New mite allergenic protein isolated from Dermatophagoides, designated
 XX PT Der HMW-map protein, useful as a vaccine for treating mite allergy.
 XX PS Claim 12; Page 120-122; 161pp; English.
 XX CC The invention relates to an isolated mite allergenic protein of
 CC Dermatophagoides, designated Der HMW-map protein, and its related nucleic
 CC acid. The Der HMW-map protein is useful for eliciting an immune response
 CC against Der HMW-map protein. The protein or a reagent comprising a non-
 CC proteinaceous epitope is useful for identifying an animal (e.g., dog,
 CC cat) susceptible to or having an allergic response to a mite. A
 CC therapeutic composition is useful for desensitising a host animal to an
 CC allergic response to a mite. The DNA and protein can be used in the
 CC detection of anti-Der HMW-map antibodies in animal fluids, and inhibition
 CC of immunoglobulin (Ig)E or Der HMW-map protein activity associated with a
 CC disease. Antibodies that bind to Der HMW-map are useful for inhibiting
 CC binding of proteins to IgE, to prevent immunocomplex formation, thus
 CC reducing hypersensitivity responses to mite allergens, and as vaccines
 CC against mite allergen hypersensitivity. Sequences AAU96314-AAU96342
 CC represent Der HMW-map polypeptides of the invention
 XX
 XX Sequence 555 AA;

Query Match 100.0%; Score 3014; DB 5; Length 555;
 Best Local Similarity 100.0%; Pred. No. 3.9e-210;
 Matches 536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIKRDNDYSKNPMRIVCVGTWVSYYHKVDPTTIEDIDPFKCTHLMYGFADIKYKTIQ 60
 Db 20 SIKRDNDYSKNPMRIVCVGTWVSYYHKVDPTTIEDIDPFKCTHLMYGFADIKYKTIQ 79
 QY 61 VFDPPQDDNHNSEKRGYERFNNLKNPELTMTISLGGWTEGSEKYSDMAANPTYRQF 120
 Db 80 VFDPPQDDNHNSEKRGYERFNNLKNPELTMTISLGGWTEGSEKYSDMAANPTYRQF 139
 QY 121 IQSVLDFLOEYKFDGLDWEYVPSRLGNPKIDKQNYLALVRELKDAFEHGYLLTAAS 180
 Db 140 IQSVLDFLOEYKFDGLDWEYVPSRLGNPKIDKQNYLALVRELKDAFEHGYLLTAAS 199
 QY 181 PGKOKIDRAYDIKELNKLFDWNNVMTYDHGGWENFYGHNAPLYKRPDTEDELHTYFNVN 240
 Db 200 PGKOKIDRAYDIKELNKLFDWNNVMTYDHGGWENFYGHNAPLYKRPDTEDELHTYFNVN 259
 QY 241 YTMHYLLNNGATRDKLVMGVPPFYGRAMSIEDRSKILKLGDPKAGMSPPGFISGEEGVL 300
 Db 260 YTMHYLLNNGATRDKLVMGVPPFYGRAMSIEDRSKILKLGDPKAGMSPPGFISGEEGVL 319
 QY 301 ELCOLFQKEEWHIQYDEYNNAPYGYNDKIWGYDDLASISCKLAFKELGVSGVMWSLE 360
 Db 320 ELCOLFQKEEWHIQYDEYNNAPYGYNDKIWGYDDLASISCKLAFKELGVSGVMWSLE 379
 QY 361 NDDFKGHCPCPNLKNVHNMINGEKNSFECILGPSTTPTTPTTPTTPTTPTTPTTPT 420
 Db 380 NDDFKGHCPCPNLKNVHNMINGEKNSFECILGPSTTPTTPTTPTTPTTPTTPTTPT 439
 QY 421 TPTTPTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPT 480


```

XX Mccall CA, Hunter SW, Weber ER;
XX
XX WPI; 2002-351888/38.
XX N-PSDB; ABK69583.
XX
XX New mite allergenic protein isolated from Dermatophagoides, designated
XX Der HMW-map protein, useful as a vaccine for treating mite allergy.
XX
XX Claim 12; Page 139-141; 161pp; English.
XX
XX The invention relates to an isolated mite allergenic protein of
XX Dermatophagoides, designated Der HMW-map protein, and its related nucleic
XX acid. The Der HMW-map protein is useful for eliciting an immune response
XX against Der HMW-map protein. The protein or a reagent comprising a non-
XX proteinaceous epitope is useful for identifying an animal (e.g., dog,
XX cat) susceptible to or having an allergic response to a mite. A
XX therapeutic composition is useful for desensitizing a host animal to an
XX allergic response to a mite. The DNA and protein can be used in the
XX detection of anti-Der HMW-map antibodies in animal fluids, and inhibition
XX of immunoglobulin (Ig)E or Der HMW-map protein activity associated with a
XX disease. Antibodies that bind to Der HMW-map are useful for inhibiting
XX binding of proteins to IgE, to prevent immunocomplex formation, thus
XX reducing hypersensitivity responses to mite allergens, and as vaccines
XX against mite allergen hypersensitivity. Sequences AAU96314-AAU96342
XX represent Der HMW-map polypeptides of the invention
XX
XX Sequence 509 AA;
XX
Query Match      82.1%; Score 2475; DB 5; Length 509;
Best Local Similarity 82.5%; Pred. No. 4.4e-171;
Matches 443; Conservative 21; Mismatches 21; Indels 52; Gaps 2;
QY 3 KRHDYKSNPMRVCVYGTWMSVYHKVDPTIEDIDPFKCTHLMYGFPAKIDEXYTIQVF 62
Db 22 KEDHNYKSNPMRVCVYGTWMSVYHKVDPTIEDIDPFKCTHLMYGFPAKIDEXYTIQVF 81
QY 63 DPYQDDHNSWEKGYERFNRLKPNELTMTISLGGWYEGSEKYSDMAANPTYRQOFIQ 122
Db 82 DPFQDDHNSWEKGYERFNRLKPNELTMTISLGGWYEGSEKYSDMAANPTYRQOFVQ 141
QY 123 SVLDFLOEYKFDGLDWEYVPGSLGNPKIDKQNYLALVRELKDAEPHCVLATAVSPG 192
Db 142 SVLDFLOEYKFDGLDWEYVPGSLGNPKIDKQNYLALVRELKEAFEPFGYLLATAVSPG 201
QY 183 KDKIDRAYDIKELNKLFDMMVMVYDYHGGWENFYGHNAFLYKRPDETDELHYFVNVT 242
Db 202 KDKIDVAYELKELNQLFDMMVMVYDYHGGWENFYGHNAFLYKRPDETDELHYFVNVT 261
QY 243 MHYYLNGATRDKLVMGVPPFYGRAWSIEDRSKLGDPAPKGMPPGPFISGEYLSYIEL 302
Db 262 MHYYLNGATRDKLVMGVPPFYGRAWSIEDRSKLGDPAPKGMPPGPFITGEGVLSYIEL 321
QY 303 COLPQKEWHIYQDEYNAPYNDKIWVGVDLILASISCKLAFKELGVSGVMVWSLEND 362
Db 322 COLPQKEWHIYQDEYNAPYNDKIWVGVDLILASISCKLAFKELGVSGVMVWSLEND 381
QY 363 DFKHCGCPKPLLNKVNMMINGDEKNSFECILGSPSTTPTPTPTPTPTPTPTPTPTPT 422
Db 382 DFKHCGCPKPLLNKVNMMINGDEKNSFECILGSPSTTPTPTPTPTPTPTPTPTPTPT 434
QY 423 TTTPSPSTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPT 482
Db 435 -----PTTIDSTSETPKYTYID 452
QY 483 GHLIKCYKEGDIPIPTTHNKHVLCYEFV---NGWVWVHMPCCPGTTCQSKLTCIGE 536
Db 453 GHLIKCYKQGYLPHTDVKYLVCEYATPNGGWVWVHMDCPKGRWHAATLKNCIQE 509

```

RESULT 11
ABP72636

ID ABP72636 standard; protein; 525 AA.

```

XX AC ABP72636;
XX
XX 11-JUN-2003 (first entry)
XX
XX Anopheles gambiae chitinase.
XX
XX Insecticide; pesticide; insect control; insect; toxin; chitinase; enzyme;
XX neuropeptide; transgenic plant; crop protection; mosquito.
XX
XX Anopheles gambiae.
XX
XX Key Location/Qualifiers
XX Peptide 1..19
XX Protein /label= Signal_peptide
XX /label= Mature_protein
XX Misc-difference 31
XX /note= "possible trypsin activation site"
XX Misc-difference 32
XX /note= "possible trypsin activation site"
XX Active-site 150..157
XX Domain 401..466
XX /note= "serine/threonine/proline-rich domain"
XX
XX WO2003014150-A2.
XX
XX 20-FEB-2003.
XX
XX 06-AUG-2002; 2002WO-GB003598.
XX
XX 08-AUG-2001; 2001GB-00019274.
XX
XX (UYDU-) UNIV DURHAM.
XX (ENVI-) DEPT ENVIRONMENT FOOD & RURAL AFFAIRS.
XX
XX Gatehouse JA, Fitches EC, Edwards JP;
XX
XX WPI; 2003-278469/27.
XX N-PSDB; AB281875.
XX
XX Fusion protein useful for combating insect pests, comprises a
XX translocating moiety comprising a plant protein capable of acting as a
XX carrier to translocate toxic moiety inside plant pathogen, and a toxic
XX moiety.
XX
XX Claim 7; Fig 15; 51pp; English.
XX
XX The present sequence is that of the mosquito Anopheles gambiae chitinase.
XX This protein is used in claimed fusion proteins of the invention. Such
XX fusion proteins comprise a translocating moiety and a toxic moiety, where
XX the translocating moiety is a plant protein (e.g. a lectin) capable of
XX acting as a carrier to translocate the toxic moiety across the gut wall
XX of a plant pathogen, and the toxic moiety is an insect-derived peptide or
XX protein capable of causing deleterious effects on growth, development,
XX reproduction or mortality in pest insects. Suitable insect peptides and
XX proteins include allatostatin, chitinase, diuretic hormone and their
XX metabolites and analogues. Polynucleotides encoding the fusion protein,
XX vectors, host cells and transgenic plants that are resistant to disease
XX are also provided. The fusion protein is target-specific, and resists
XX degradation in the insect gut
XX
XX Sequence 525 AA;

```

Query Match 33.4%; Score 1007; DB 6; Length 525;
Best Local Similarity 39.5%; Pred. No. 1.5e-64;
Matches 210; Conservative 86; Mismatches 178; Indels 58; Gaps 12;

QY 6 HNDYKSNPMRVCVYGTWMSVYHKVD-PYTIEDIDPFKCTHLMYGFPAKIDEXYTIQVDP 64
Db 23 HXASAEGKKVVCYVGTWAVYRPGNGRVDIEHIDPSLCTHLMYGFGINE-DATVRIIDP 81
QY 65 YQDDHNSWEKGYERFNRLKPNELTMTISLGGWYEGSEKYSDMAANPTYRQOFIQSV 124

Db 82 YLDLEEN-WRGCHIKRFGVGLKNVPGGLKTLAAGWNEGRKRSAMAASGELRKRISDC 140
Qy 125 LDFQYKFGDLDWEYPSRSLGNPKIDKONYALVRELKDAFEPHGYLLTAAVSPGKD 184
Db 141 VAFQQRHGFQDGLDWEYPAQRDGNPLIDRDNAQLVEEMREBFDHYGLLLTAAVASVEF 200
Qy 185 KIDRAYDIKELNKLFDWNNVTYDYGWENFYGHNAPLYKRPDETDHLYFNVNYTMH 244
Db 201 SAGVSYDIPRISKSFHFLNVMVDMHGAWDSYCCINAPLYRGSADTTDLRGQINVASIH 260
Qy 245 YLLNNGATRDKLVMGVFPYGRANSIEDRSKLKGDPAKMSPPGFTSGEGVLSTELCQ 304
Db 261 FWLAQGGCTGRKLVIGILYGRNFTLASAANTQIGAPTVCGGTVCRTREFGVNGYNEFCE 320
Qy 305 LFOKEEWHIOVDEYINAPYGVNDKIWGYDDLASISCKLAFKLKELGVGMWWSLNDDF 364
Db 321 KLATEAWDLWSSEQQVYAVRNQWGVYDLSVQLKVKLLDQGLGGAMWSLSTDF 380
Qy 365 KGHG-GPNKPLLNKVNMMINGDEKNSFECILGFTSTTPTTPTTPTTPTTPTTPTTPT 423
Db 381 LGVCGGGRYELMHEIRSLVNGGT-----FSTTTPPSVAPT-----STVAGTTT 426
Qy 424 TTPSPPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPT 483
Db 427 TTPGANPGTQPTT--SDAPNHTTSTTEGNGPTTRPPSG-----DQ 468
Qy 484 HLKCY--KSGDIPHPNINHLKLV-----EFVNGWVHLMPCPPGTIW 526
Db 469 ---PCAGRGYGFVHPHTNCARYICLTADTYEFT-----CPPGTFL 507

RESULT 12
ABBS58595
ID ABBS58595 standard; protein; 4498 AA.
XX AC ABBS58595;
XX DT 26-MAR-2002 (first entry)
XX DE Drosophila melanogaster polypeptide SEQ ID NO 2577.
XX KW Drosophila; developmental biology; cell signalling; insecticide;
XX KW pharmaceutical.
XX OS Drosophila melanogaster.
XX PN WO200171042-A2.
XX PD 27-SEP-2001.
XX PF 23-MAR-2001; 2001WO-US009231.
XX PR 23-MAR-2000; 2000US-0191637P.
XX PR 11-JUL-2000; 2000US-00614150.
XX PA (PEKE) PE CORP NY.
XX PI Venter JC, Adams M, Li PWD, Myers EW;
XX WPI; 2001-656860/75.
XX DR N-PSDB; ABL02698.

PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions.
XX Disclosure; SEQ ID NO 2577; 21pp + Sequence Listing; English.
XX CC The invention relates to an isolated nucleic acid detection reagent
XX capable of detecting 1000 or more genes from Drosophila. The invention is
XX useful in developmental biology and in elucidating cell signalling and
XX cell-cell interactions in higher eukaryotes for the development of

CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC ABB72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 4498 AA;
Query Match 28.2%; Score 848.5; DB 4; Length 4498;
Best Local Similarity 34.9%; Pred. No. 7.3e-52;
Matches 197; Conservative 81; Mismatches 180; Indels 107; Gaps 19;
Qy 15 RIVCVGVTSVYH-----KVDPTIIDIPEKCTHLMY---GPAKIDVYKTIQVDPYQD 67
Db 53 RVVCYTWSVYRPTAKFNP---QNIPLYLTHLVYAFGGFTKDNQWK---PDKYQD 105
Qy 68 DNHNSWEKRGYERFNNRLKNPELTMTISLGGWVEGSEKYSDMAANPYRQOFTQSVLDF 127
Db 106 -----IEGGYAKFTGLATYKQLKTMIAIGWNEASSRFPPLVASNRRQOFTKILKF 160
Qy 128 LOEYKFDGLDLDWEYPSRSLGNPKIDKONYALVRELKDAFEPHG-----YLLTAVS 180
Db 161 LEQNHFDGIDLDWEYFAHREGGKSRDRDNYAQFVQELKAEFEREAETGRTRLLTMAVP 220
Qy 181 PKDKIDRAYDIKELNKLFDWNNVTYDYGWENFYGHNAPLYKRPDETDHLY----F 237
Db 221 AGIEYIDKGYDVPKLNKYLDWFLNLYTDFHSSHEPSVNHHAFLYSL--EEDSEYNYDAEL 278
Qy 238 NVNYTMHYLNNAGTRDKLVNGVFPYGRANSIEDRSKLKGDPAKMSPPGFTSGEGVL 297
Db 279 MIDYSIKYLLXAGADRDKLVIGIPYGRSYTLNEESTELGAPAEQGEQGDATREKGYL 338
Qy 298 SYIELCQLFOKE-EWH-IQYDEYINAPYGVNDKIWGYDDLASISCKLAFKLKELGVSGVM 355
Db 339 AYYELCQLKDDPEWTVVQPNANVMGYAVRNQWGVYDDEAIYKKAAYVVAQGLGIM 398
Qy 356 VWSLENDDFKHC-GPNKPLLNKVNMMINGDEKNSFECILGFTSTTPTTPTTPTTPTTPTT 414
Db 399 FWAINDDDFRGTGCKGPKYPLTEAA-----KEAMVEALGLGINEVAKPSGPKPSRSR 450
Qy 415 T-----TPSFTT---PTTSPPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTT 443
Db 451 SRDNASNRNLNGKTEAPLSRRPSATRRPAVSSTQAPP--PSTFKLTEAGSSLYIGG 508
Qy 444 -PSPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTT 502
Db 509 RASTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPT 542
Qy 503 YLVCEFYNG-----GWWVHIMPCPPG 523
Db 543 YYWC-LDSGPGSLGIVAHMFTCPG 566

RESULT 13
ABP72634
ID ABP72634 standard; protein; 467 AA.
XX AC ABP72634;
XX DT 23-OCT-2003 (revised)
XX DT 11-JUN-2003 (first entry)
XX DE Prawn chitinase.
XX KW Insecticide; pesticide; insect control; insect; toxin; chitinase; enzyme;
XX KW neuropeptide; transgenic plant; crop protection; prawn.
XX OS Marsupenaeus japonicus.
XX FH Key Location/Qualifiers
XX FT Active-site 118..125
XX

[illegible]

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OM protein - protein search, using sw model

Run on: March 22, 2004, 06:39:53 ; Search time 107.855 Seconds
(without alignments)
1568.003 Million cell updates/sec

Title: US-09-662-293-21
Perfect score: 3014
Sequence: 1 SIKRDNDYSKNPBRIVCV.....IMPCPPGTWQCKLTICGE 536

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : SPTREMBL 25:*
- 1: sp_archaea:*
 - 2: sp_bacteria:*
 - 3: sp_fungi:*
 - 4: sp_human:*
 - 5: sp_invertebrate:*
 - 6: sp_mammal:*
 - 7: sp_mhc:*
 - 8: sp_organelle:*
 - 9: sp_phage:*
 - 10: sp_plant:*
 - 11: sp_rodent:*
 - 12: sp_virus:*
 - 13: sp_vertibrate:*
 - 14: sp_unclassified:*
 - 15: sp_rvirus:*
 - 16: sp_bacteriap:*
 - 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3014	100.0	555	Q9U6R7	Q9U6R7 dermatophag
2	1007	33.4	525	O44079	O44079 anopheles g
3	938	31.1	431	Q81SH5	Q81SH5 araneus ven
4	869	28.8	1635	O17412	O17412 aedes aegyp
5	848.5	28.2	4498	Q9W2Z3	Q9W2Z3 drosophila
6	842	27.9	2838	Q8MP05	Q8MP05 tenebrio mo
7	837.5	27.8	467	O15993	O15993 penaeus jap
8	837.5	27.8	595	Q9VFR3	Q9VFR3 drosophila
9	831.5	27.6	467	Q81TU3	Q81TU3 penaeus van
10	830.5	27.6	460	Q9W2M7	Q9W2M7 drosophila
11	826	27.4	544	Q9GQC4	Q9GQC4 bombyx mori
12	823	27.3	488	Q30W34	Q30W34 bufo japoni
13	821.5	27.3	557	Q8MTK0	Q8MTK0 choriostoneu
14	819	27.2	543	Q9GR93	Q9GR93 bombyx mori
15	819	27.2	543	Q9GV05	Q9GV05 bombyx mori
16	819	27.2	565	P90710	P90710 bombyx mori

17	818	27.1	566	5	Q8WR52	Q8WR52 bombyx mori
18	811	26.9	565	5	Q9GPG9	Q9GPG9 bombyx mand
19	808	26.8	574	5	O17411	O17411 aedes aegyp
20	801.5	26.6	483	5	Q23737	Q23737 chelonus sp
21	801	26.6	552	5	Q9GV44	Q9GV44 spodoptera
22	797	26.4	572	5	Q26042	Q26042 penaeus jap
23	790	26.2	620	5	Q9Y0D4	Q9Y0D4 penaeus mon
24	779.5	25.9	553	5	P91731	P91731 hyphantria
25	775	25.7	470	13	Q803B7	Q803B7 brachydanio
26	755.5	25.1	474	5	Q86L22	Q86L22 lutzomyia l
27	754	25.0	500	13	Q7ZV48	Q7ZV48 brachydanio
28	738	24.5	466	4	Q13231	Q13231 homo sapien
29	732.5	24.3	387	4	Q9H3V8	Q9H3V8 homo sapien
30	732	24.3	482	13	Q8AV87	Q8AV87 gallus gall
31	730.5	24.2	472	6	Q95M17	Q95M17 bos taurus
32	729.5	24.2	473	11	Q99PH2	Q99PH2 mus musculu
33	727.5	24.1	472	11	Q9JLN1	Q9JLN1 mus musculu
34	727.5	24.1	473	11	Q9D803	Q9D803 mus musculu
35	723.5	24.0	688	5	Q8MS85	Q8MS85 drosophila
36	722.5	24.0	1013	5	Q960M0	Q960M0 drosophila
37	717	23.8	527	5	P91773	P91773 penaeus jap
38	711	23.6	460	5	Q8WS95	Q8WS95 glossina mo
39	710	23.6	484	5	Q9W092	Q9W092 drosophila
40	708.5	23.5	476	4	Q9BZP6	Q9BZP6 homo sapien
41	702.5	23.3	929	5	Q8MY79	Q8MY79 haemaphysal
42	702.5	23.3	983	5	Q9VZV2	Q9VZV2 drosophila
43	687	22.8	381	11	Q99J84	Q99J84 mus musculu
44	687	22.8	389	11	Q8BKL8	Q8BKL8 mus musculu
45	677	22.5	461	5	O01936	O01936 chironomus

ALIGNMENTS

RESULT 1

Q9U6R7 PRELIMINARY; PRT; 555 AA.

AC Q9U6R7

DT Q9U6R7; 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

DE 98kDa HDM allergen.

OS Dermatophagoides farinae (House-dust mite).

OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;

OC Acariiformes; Sarcotiformes; Astigmata; Psoroptidia; Analgoidea;

OC Pyroglyphidae; Dermatophagoides.

OX NCBI_TaxID=6954;

EN [1]

RP SEQUENCE FROM N.A.

RA Weber E.R., Hunter S., Stedman K., McCall C.;

RT "Cloning and Characterization of a 98 kDa Allergen from Dermatophagoides farinae";

RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF178772; AAD52672.1; -

DR GO; GO:0005576; C:extracellular; IEA.

DR GO; GO:0008061; F:chitin binding; IEA.

DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.

DR GO; GO:0005975; P:carbohydrate metabolism; IEA.

DR GO; GO:0006030; P:chitin metabolism; IEA.

DR InterPro; IPR002557; Chitin bind PerA.

DR	InterPro; IPR001223; Glyco Hydro 18.
DR	InterPro; IPR001579; Glyco hydro 18AS.
DR	Pfam; PF00704; Glyco_hydro_18; 1-
DR	ProDom; PD000471; Glyco_hydro_18; 1.
DR	SMART; SM00494; ChitBD2; 1.
DR	SMART; SM00636; Glyco 18; 1.
DR	PROSITE; PS01095; CHITINASE_18; 1.
KW	Glycosidase; Hydrolase.
SQ	SEQUENCE 555 AA; 63238 MW; OE4564A1A459B30B CRC64;
Query Match	100.0%; Score 3014; DB 5; Length 555;
Best local similarity	100.0%; Pred. No. 2.2e-180;
Matches 536; Conservative	0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIKRDNDYSKNMEIVCVGTWTSVYHKVDPTIEDIDPFKCTHLMYGFADIDYKTYIQ 60
 DB 20 SIKRDNDYSKNMEIVCVGTWTSVYHKVDPTIEDIDPFKCTHLMYGFADIDYKTYIQ 79
 QY 61 VDPYODDNDHNSWEKRGYERFNNLRLKNPELTMTISLGGWYEGSEKYSMDAANTYRQOF 120
 DB 80 VDPYODDNDHNSWEKRGYERFNNLRLKNPELTMTISLGGWYEGSEKYSMDAANTYRQOF 139
 QY 121 IQSVLDFPQYKFDGLDWEYPSGRNPKIDKQNYLALVRELKDAPEPHGYLLTAAS 180
 DB 140 IQSVLDFPQYKFDGLDWEYPSGRNPKIDKQNYLALVRELKDAPEPHGYLLTAAS 199
 QY 181 PKQKIDRAYDIKELNKLFDWNVMTYDHGGWENFYGHNAPLYKRPDETDELHTYFNVN 240
 DB 200 PKQKIDRAYDIKELNKLFDWNVMTYDHGGWENFYGHNAPLYKRPDETDELHTYFNVN 259
 QY 241 YTMHYLLNNGATRDKLVMGVPPFYGRAWSIEDRSKLKLGDPKAGMSPPGFISGEGVLSYI 300
 DB 260 YTMHYLLNNGATRDKLVMGVPPFYGRAWSIEDRSKLKLGDPKAGMSPPGFISGEGVLSYI 319
 QY 301 ELQCFQKEEWHIOYDEYNAPYGNKIDKQNYLALVRELKDAPEPHGYLLTAAS 360
 DB 320 ELQCFQKEEWHIOYDEYNAPYGNKIDKQNYLALVRELKDAPEPHGYLLTAAS 379
 QY 361 NDDKRGHCGPKNPLKVNMMINGDEKNSFECILGSPSTTPTPTPTPTPTPTPTPTPTPT 420
 DB 380 NDDKRGHCGPKNPLKVNMMINGDEKNSFECILGSPSTTPTPTPTPTPTPTPTPTPTPT 439
 QY 421 TPT 480
 DB 440 TPT 499
 QY 481 VDGLIKCYKEGDI PHTPT 536
 DB 500 VDGLIKCYKEGDI PHTPT 555

RESULT 2
 O44079 ID O44079 PRELIMINARY; PRT; 525 AA.
 AC O44079;
 DT 01-JUN-1998 (TremBLrel. 06, Created)
 DT 01-JUN-1998 (TremBLrel. 06, Last sequence update)
 DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
 DE Chitinase.
 GN AGCHI-1.
 OS Anopheles gambiae (African malaria mosquito).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
 OX NCBI_TaxID=7165;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Gut;
 RX MEDLINE=98030563; PubMed=9360958;
 RA Shen Z., Jacobs-Lorena M.;
 RT "Characterization of a novel gut-specific chitinase gene from the
 human malaria vector Anopheles gambiae.";
 RL J. Biol. Chem. 272:28895-28900(1997).
 DR EMBL; AF008575; AAB87764.1; -;
 DR FIR; T44445; T44445.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0008061; F:chitin binding; IEA.
 DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR GO; GO:0006030; P:chitin metabolism; IEA.
 DR InterPro; IPR002557; Chitin bind_Pera.
 DR InterPro; IPR001223; Glyco_hydro_18.
 DR InterPro; IPR001579; Glyco_hydro_18AS.
 DR Pfam; PF01607; CSM_14; 1.
 DR Pfam; PF00704; Glyco_hydro_18; 1.
 DR ProDom; PD000471; Glyco_hydro_18; 1.
 DR SMART; SM00494; ChtBD2; 1.

DR SMART; SM00636; Glyco_18; 1.
 DR PROSITE; PS01095; CHITINASE_18; 1.
 KW Glycosidase; Hydrolase.
 SQ SEQUENCE 525 AA; 57211 MW; 3234360EEFF36165 CRC64;
 Query Match 33.4%; Score 1007; DB 5; Length 525;
 Best Local Similarity 39.5%; Pred. No. 5.2e-55;
 Matches 210; Conservative 86; Mismatches 178; Indels 58; Gaps 12;
 QY 6 HNDYKSNPKRIVCYCVGTWTSVYHKVDPTIEDIDPFKCTHLMYGFADIDYKTYIQVDP 64
 DB 23 HKAASAEKGVYCVGTWTSVYHKVDPTIEDIDPFKCTHLMYGFADIDYKTYIQVDP 81
 QY 65 YQDNNHNSWEKRGYERFNNLRLKNPELTMTISLGGWYEGSEKYSMDAANTYRQOF 124
 DB 82 YLDLEN-WGRGHIKRFVGLKKNVGPGLKTLAIGWNEGRKFSMAAASGELRKRISDC 140
 QY 125 LDFLQBYKFDGLDWEYPSGRNPKIDKQNYLALVRELKDAPEPHGYLLTAASVPGKD 184
 DB 141 VAPCQRHGFDGLDWEYPAQRDGNPLIDRDNHAQLVEEMRBEFDHYGLLLTAASVVEF 200
 QY 185 KIDRAYDIKELNKLFDWNVMTYDHGGWENFYGHNAPLYKRPDETDELHTYFNNTWH 244
 DB 201 SAGVSYDIIPRISKSPFLNVMYDMEGAWDSYGINAPLYRGSADTTDLGQINNVASIH 260
 QY 245 YLLNNGATRDKLVMGVPPFYGRAWSIEDRSKLKLGDPKAGMSPPGFISGEGVLSYIELCQ 304
 DB 261 FWLAQCTGRKLVIGPLIGRNFTLASAANTQIGAPTGGTVGRTREPGWGVNEFCE 320
 QY 305 LFOKEBWHIOYDEYNAPYGNKIDKQNYLALVRELKDAPEPHGYLLTAASVPGKD 364
 DB 321 KLATEAWDLRWSEQQVPYAVRNNQWGYDDLSVQLVKYLLDQGLGGMWVSLTDDF 380
 QY 365 KGHG-GEKPLNKNVMMINGDEKNSFECILGSPSTTPTPTPTPTPTPTPTPTPTPTPT 423
 DB 381 LGVCGGRVPLMEIRSLVNGGT-----PSTTTPPSVAPT-----STVAPGTTT 426
 QY 424 TTPSPPT 483
 DB 427 TPTGANPGTQPPT--SDAPNHTTSTTTEGPNPTPTPTPTPTPTPTPTPTPTPTPTPTPT 507
 QY 484 HLIKCY--KEGDIPHTPT 526
 DB 469 ---PCAGRGYGFVPHPTNCAARYICLTADTYEFT-----CPGTLF 507

RESULT 3
 Q81SH5 ID Q81SH5 PRELIMINARY; PRT; 431 AA.
 AC Q81SH5;
 DT 01-MAR-2003 (TremBLrel. 23, Created)
 DT 01-MAR-2003 (TremBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
 DE Chitinase.
 OS Araneus ventricosus.
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
 OC Araneomorphae; Entelegynae; Araneioidea; Araneidae; Araneus.
 OX NCBI_TaxID=182803;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Han J.H., Kim S.R., Sohn H.D., Jin B.R.;
 RT "Molecular cloning of a cDNA encoding the chitinase from the spider,
 Araneus ventricosus.";
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY120879; AAN39100.1; -;
 DR GO; GO:0016787; F:hydrolase activity; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro; IPR001223; Glyco_hydro_18.
 DR InterPro; IPR001579; Glyco_hydro_18AS.
 DR Pfam; PF00704; Glyco_hydro_18; 1.
 DR ProDom; PD000471; Glyco_hydro_18; 1.
 DR SMART; SM00636; Glyco_18; 1.
 DR PROSITE; PS01095; CHITINASE_18; 1.

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DR SMART; SM00494; ChtBD2; 3.
DR DR SMART; SM00636; GlyCO 18; 3.
DR PROSINE; PS01095; CHITINASE 18; 3.
KW Hydrolase; Glycosidase; Chitin degradation; Glycoprotein;
KW Multigene family.
FT CARBOHYD 192 192 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 322 322 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 749 749 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 890 890 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1338 1338 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1479 1479 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 1635 AA; 185993 MW; EA116F83AAC129FA CRC64;

Query Match 28.8%; Score 869; DB 5; Length 1635;
Best Local Similarity 34.3%; Pred. No. 8.5e-46;
Matches 196; Conservative 95; Mismatches 196; Indels 84; Gaps 18;

Qy 2 IKRDNDYSKNPM-----RIVCVGVTWSVYHKVD-PYTIEDIDPFCXTHLMYGFKAIDE 54
      ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
Db 650 INKTSNQDNIAESVDYKVCVYFTNVAWROGNGKYLPEIDALCTHIVYGFVALDR 709
      ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::

Qy 55 YKTIQVDFPYQDDNHSW---EKRGYERENNURLKNPELTTMISLGGWYEGS-EKYSDM 110
      ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
Db 710 DLRIK-----PHDSWADINRRYFERYVYKKGKKVT--VALGGMNDSAGDKYSRL 759
      ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::

Qy 111 AAMPTRYRQQPIQSVLDPDLQYKEFGDGLDWEYPSGRIGNPK----IDKNYLALVRELKD 166
      ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
Db 760 VRSAARQKFIADVVAIEKYKGFGLDGLDWEYFVPCVQVDCCKGFSDEKGFASLVVLSQ 819
      ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::

Qy 167 AFEPHGYYLLTAAPVSPGKKIDRAYDIKELNKLFDNMVMTYDYHGQWENFYGHNAPLYKR 226
      ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
Db 820 AFKPKGLLSSAYSPSKVDEGVVVLTSDYMDWTAVMAVDYHGQWDKXTGHVAPMYEH 879
      ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::

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227 PDETDLHITFYNNVYTHYLLNNGATKDLVLMGVPFYIGRAWSJEDRSKLLGDPAGKMSNP 286
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
880 PDDPDKT---FNAFNFTIHYWIEKGADPRKLVGMGMPYQGSFLADNKEHGLNAKTYGGGE 936
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
287 PGIISGEGVLSVIELCOLFQKEWHIODEYTN-APYGVNDKIWIYGVDDLASISCKLAF 345
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
937 AGESTRARGFLSYEICANTRNKKWTIVARDKGRMGFPYAKGQWVSFDDQVVMIRHKSEY 996
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
346 LKELGVGVVMVSLENDDFKHCYG-PKNPLLNKVNHNMGDEKNSPECIL--CPSTTTTPT 402
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
997 VKAMGLGGAMIWALDLDFFNLDCOEYPLLRITNRLVNRYPGGRCVLEKFEQREPR 1056
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
403 PTTTPTPTTTTPTPTSPPTTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTT 462
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1057 PTPPTTS-----TTPETTERSTTSTRITWTITTT--TTTRPPTTTTRRTTSAR 1104
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
463 PSPTTTEHTSETPKY-----TTYVDGHLIKCYKEGDIPHPTNIHKYLVCSEFVNGGW 513
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1105 PTYTIT---NVFSYQEIANEVDEPCTDGRLF-----VPHTDCNKYIICQYGK--- 1150
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
514 WVHIMPCPPGTIW-----COEKLT 532
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1151 ----LCPGGLYMSVDHCDWPGQSTNCRNKQT 1176
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 5
Q9W223 PRELIMINARY; PRT; 4498 AA.
AC Q9W223;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE CG2989 protein.
GN CG2989.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI TaxID=7227.

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RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=Berkley;
RX      MEDLINE=20196006; PubMed=10731132;
RA      Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA      Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA      Sutton R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA      Georger G.A., Wortman J.R., Randell M.D., Zhang Q., Chen L.X.,
RA      Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA      Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA      Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA      Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA      Beeson K.Y., Benson P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA      Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA      Burris K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA      Cherry J.M., Delcher S., Dahlke C., Davenport L.B., Davies P.,
RA      de Pablo J.M., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA      Dodson K., Doup I.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA      Durbin K.J., Evangelista C.C., Ferraz C., Fertiera S., Fleischmann W.,
RA      Fouts D.C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA      Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA      Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA      Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
RA      Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA      Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA      Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA      Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA      Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA      Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA      Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA      Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA      Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA      Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA      Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA      Svitek R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA      Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
RA      Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA      Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA      Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA      Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT      "The genome sequence of Drosophila melanogaster."
RL      Science 287:2185-2195(2000).
DR      EMBL; AE003449; AAF46544.1; -.
DR      FlyBase; FBgn0030171; CG2989.
DR      GO; GO:0005575; C:extracellular; IEA.
DR      GO; GO:0008061; F:chitin binding; IEA.
DR      GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR      GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR      GO; GO:0006030; P:chitin metabolism; IEA.
DR      InterPro; IPR002557; Chitin_bind_PeA.
DR      InterPro; IPR001223; Glyco_hydro_18.
DR      Pfam; PF01607; CBM_14; 1.
DR      Pfam; PF00704; Glyco_hydro_18; 1.
DR      ProDom; PD000471; Glyco_hydro_18; 1.
DR      SMART; SM00494; ChtBD2; 1.
DR      SMART; SM00636; Glyco_18; 1.
DR      PROSITE; PS01095; CHITINASE_18; 1.
KW      Glycosidase; Hydrolase.
SQ      SEQUENCE 4498 AA; 493096 MW; AEE65CE0AAB25489 CRC64;

Query Match      28.2%; Score 848.5; DB 5; Length 4498;
Best Local Similarity 34.9%; Pred. No. 5.4e-44;
Matches 197; Conservative 81; Mismatches 180; Indels 107; Gaps 19;

QY      15 RIVCVGTWVSVVH-----KVDPTVIEDIDPKCTHLMY---GFAKIDVKYTIQVDFPYQD 67
DB      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY      68 DNHNSWKRGYERFNNLRKLPKLTMLISLGWTEGSEKYSKDMAANPYRQOQIQSVLDF 127
DB      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB      106 -----IEQGGYAKFTGLTKYNKQLKMTAIGWNEASSRPFPLVASNRRQOQFNILKF 160

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RESULT 6

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Q8MP05      Q8MP05      PRELIMINARY;      PRT; 2838 AA.
AC      Q8MP05;
DT      01-OCT-2002 (T-EMBLrel. 22, Created)
DT      01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
DT      01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE      Chitinase precursor (SC 3.2.1.14).
GN      CHITS.
OS      Tenebrio molitor (Yellow mealworm).
OC      Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC      Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
OC      Tenebrionidae; Tenebrio.
OX      NCBI_TaxID=7067;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Royer V., Fraichard S., Bouhin H.;
RT      "A Novel putative insect Chitinase with multiple catalytic domains :
RT      hormonal regulation during metamorphosis."
RL      Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AJ487081; CAD31740.4; -.
DR      GO; GO:0005576; C:extracellular; IEA.
DR      GO; GO:0008061; F:chitin binding; IEA.
DR      GO; GO:0008843; F:endochitinase activity; IEA.
DR      GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR      GO; GO:0006520; P:amino acid metabolism; IEA.
DR      GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR      GO; GO:0006030; P:chitin metabolism; IEA.
DR      InterPro; IPR002557; Chitin_bind_PeA.
DR      InterPro; IPR001223; Glyco_hydro_18.
DR      InterPro; IPR001579; Glyco_hydro_18AS.
DR      InterPro; IPR000634; s/T dehydratase_BS.
DR      Pfam; PF01607; CBM_14; 5.
DR      Pfam; PF00704; Glyco_hydro_18; 5.
DR      ProDom; PD000471; Glyco_hydro_18; 5.
DR      SMART; SM00494; ChtBD2; 5.
DR      SMART; SM00636; Glyco_18; 5.
DR      PROSITE; PS01095; CHITINASE_18; 3.
DR      PROSITE; PS00165; DEHYDRATASE_SER_THR; 1.
KW      Signal; Hydrolase; Glycosidase.

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RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA April J.P., Abayani A., An H.-J., Andrews-Famknoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P.,
RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Fabois B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hoskin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Williams S.M., Woodard D.A., Weinstock G.M., Weissbach J.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nunoo J., Pacle J., Paragas V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003701; AAF54987.1; -
DR EMBL; AV061553; AAL29101.1; -
DR FlyBase; FBgn038180; CG9307.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008061; F:chitin binding; IEA.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0006030; P:chitin metabolism; IEA.
DR InterPro; IPR002557; Chitin_bind_Pera.
DR InterPro; IPR001223; Glyco_hydro_18.
DR Pfam; PF01607; CBM_14; 1.
DR Pfam; PF00704; Glyco_hydro_18; 1.
DR ProDom; PD000471; Glyco_hydro_18; 1.
DR SMART; SM00494; ChtBD2; 1.
DR SMART; SM00636; Glyco_18; 1.
DR PROSITE; PS01095; CHITINASE_18; 1.
KW Glycosidase; Hydrolase.
SQ SEQUENCE 595 AA; 67050 MW; 8DC8469D3F732593 CRC64;
Query Match 27.8%; Score 837.5; DB 5; Length 595;
Best Local Similarity 35.2%; Pred. NO. 2.4e-44;
Matches 201; Conservative 84; Mismatches 199; Indels 87; Gaps 22;

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Db 247 WLKAGAPAEKLIIGVPIYGRSFTLATAEGNQGAPHICKIGKIAGNYSGREPGLVGNELCEM 306
Qy 306 FQKEBHIQDYENYAPYNDKIWGYDDLASICKLAFKLXELGSGVGMVWSLENDDFK 365
Db 307 MEREEWQKEATQVYAYRQRWGYEDPRSLAKAQVMDNHLGIMWSLESDDFR 366
Qy 366 GHCGPK-NPLLKNVHNMINGDEKNSFCILGPSTTTPTTTPTTTPTTTPTTTPTTTPTTT 424
Db 367 GTCQQQPYPLHLINRVLFGG----- 387
Qy 425 TPTSTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPT 482
Db 388 -----NTPSGLTTESNRSPSGFSGPAD 411
Qy 483 GHLLIKYKEGDIPHPTNIHKYLVCFEVNGVWVHIMPCCPGTIWCQKLC7C 533
Db 412 A-----PAGVIRPDNCSKEYVC-----SGKTHNFDPCPSGLNFDLDTKSC 452

RESULT 11
Q9GQC4
ID Q9GQC4 PRELIMINARY; PRT; 544 AA.
AC Q9GQC4;
DT 01-MAR-2001 (TremBLrel. 16, Created)
DT 01-MAR-2001 (TremBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Chitinase.
OS Bombyx mori (silk moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
OC Bombycidae; Bombyx.
OX NCBI_TaxID=7091;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Shunrei x Showgetsu;
RX MEDLINE=20545518; PubMed=10984482;
RA Mikitani K., Sugasaki T., Shimada T., Kobayashi M., Gustafsson J.A.;
RT "The Chitinase Gene of the Silkworm, Bombyx mori, Contains a Novel Tc-
RT like Transposable Element.";
RL J. Biol. Chem. 275:37725-37732(2000).
DR EMEL; AF273695; AAG37105.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008061; F:chitin binding; IEA.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0006030; P:carbohydrate metabolism; IEA.
DR InterPro; IPR002557; Chitin bind PerA.
DR InterPro; IPR001223; Glyco_hydro_18.
DR InterPro; IPR001579; Glyco_hydro_18AS.
DR Pfam; PF01607; CEM_14; 1.
DR Pfam; PF00704; Glyco_hydro_18; 1.
DR ProDom; PD000471; Glyco_hydro_18; 1.
DR SMART; SM00494; ChtBD2; 1.
DR SMART; SM00636; Glyco_18; 1.
DR PROSITE; PS01095; CHITINASE_18; 1.
KW Glycosidase; Hydrolase.
SQ SEQUENCE 544 AA; 61069 MW; 89872DFC1DA23753 CRC64;

Query Match 27.4%; Score 826; DB 5; Length 544;
Best Local Similarity 27.3%; Pred. No. 1.1e-43;
Matches 199; Conservative 71; Mismatches 209; Indels 54; Gaps 17;

Qy 15 RIVCVGTWSVYHK-VDPYTTIEDIPFKCTHLMYGFKAIDYKYTIQVDPYQDNNHNSW 73
Db 26 RIVCVFSNWAYRPGVGRYGIEDIPVDICTHLYISFGVTEKSEVLIIIDPDL-----V 80
Qy 74 BKGVERNNLRLKNPELTTMISGGVYEGSEKTSMDAANPTYQQIISVLDPLQYKF 133
Db 81 DKSGRNFTSLRSKHPDVKFMVAVGWAEGSGSKYSHMVAQKSTRMSFRSVDFLKKYDF 140
Qy 134 DGLDLDEYPGSR-LGNPKIDKQNYLAVRELKDAF--EPHYLLTAAVSPGKDIDRAY 190
Db 134 DGLDLDEYPGSR-LGNPKIDKQNYLAVRELKDAF--EPHYLLTAAVSPGKDIDRAY 190
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Db 141 DGLDLDEYPGAADRGGSFSDKDEFLYFVQELKRAFIADRGWELTAAPLANFLMBGY 200
Qy 191 DIKELNKLFDMMNVTYDHYHGWNFYGHNAFLYKRPDETDELHTYFNNVTMYYLNNG 250
Db 201 HYPELCQELDAIHVMYSYDLRGWAGFADVHSPLKYKRPD-QWAYEKLNVNDGLNLWEEKG 259
Qy 251 ATRDLKLVGVPPYGRASIED-----RSKLKLGDPKAGMSPPGFISSGEEGVLSY 299
Db 260 CFTNKLVLVGIPIFYGRSFTLSAGNNNYGLTVINKEAGGDPAPYTNATGF-----WAY 312
Qy 300 IELCQLFQKE--EWHIOYDEVNAPYGYNDKIWGYDDLASICKLAFKLXELGSGVGMV 357
Db 313 YEICTEVADAGSGWTWKNDKFCYAYKGTQWGYEDPRSVIEKMWIKKXGVLGATW 372
Qy 358 SLENDDFKHGCHGPKNPLKNVHNMINGDEKNSFCILGPSTT---TPTPTPTPTPTPTPT 414
Db 373 AIDMDDFKGLGGEENPLIKLLH-----KHMSTVTPPARTGHATPTPEW--ARPPSTP 423
Qy 415 TPTSTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPT 474
Db 424 SDPESEGDPI-----PTTTTTPKPTTTRTTARPT---TTTTKVPHGTTEDFDINVRPEVE 477
Qy 475 PKYTTYVDGHLIKCYKEGD-IPHPTNIHKYLVCFEVNGVWVHIMPCCPGTIW 526
Db 478 PPTENEVDNADV-CNSEDDYVDPKCKSKYWRG--VNGEGVQ--PSCQPGTIIF 525
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RESULT 12

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Q90W34
ID Q90W34 PRELIMINARY; PRT; 488 AA.
AC Q90W34;
DT 01-DEC-2001 (TremBLrel. 19, Created)
DT 01-DEC-2001 (TremBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Toad pancreatic chitinase (EC 3.2.1.14).
GN TPCASB.
OS Bufo japonicus (Japanese toad).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Bufo.
OX NCBI_TaxID=8387;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Pancreas;
RA Oshima H.;
RL Thesis (2001), Department of Department of Biology, Waseda University,
RL Tokyo, Japan.
DR EMEL; AJ345054; CAC87888.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008061; F:chitin binding; IEA.
DR GO; GO:0008843; F:endochitinase activity; IEA.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0006030; P:chitin metabolism; IEA.
DR InterPro; IPR002086; Aldehyde dehydr.
DR InterPro; IPR002557; Chitin bind PerA.
DR InterPro; IPR001223; Glyco_hydro_18.
DR InterPro; IPR001579; Glyco_hydro_18AS.
DR Pfam; PF01607; CEM_14; 1.
DR Pfam; PF00704; Glyco_hydro_18; 1.
DR ProDom; PD000471; Glyco_hydro_18; 1.
DR SMART; SM00494; ChtBD2; 1.
DR SMART; SM00636; Glyco_18; 1.
DR PROSITE; PS00070; ALDEHYDE DEHYDR_CYS; 1.
DR PROSITE; PS01095; CHITINASE_18; 1.
KW Glycosidase; Hydrolase; Signal.
FT SIGNAL 1 48
FT CHAIN 19 488 TOAD PANCREATIC CHITINASE.
SQ SEQUENCE 488 AA; 54319 MW; E75E1AD3CB2B4919 CRC64;
```

Query Match 27.3%; Score 823; DB 13; Length 488;

Best Local Similarity 34.7%; Pred. No. 1.5e-43;

Matches 186; Conservative 88; Mismatches 174; Indels 88; Gaps 18;

[illegible]

RESULT 13

Q8MTK0 PRELIMINARY; PRT; 557 AA.
Q8MTK0;
Q8MTK0 AC
01-OCT-2002 (TReMBLrel_22, Created)
01-DEC-2002 (TReMBLrel_22, Last sequence update)
01-OCT-2003 (TReMBLrel_25, Last annotation update)
DE Chitinase.
CHIT.
OOS Choristoneura fumiferana (Spruce budworm).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Tortricidae; Tortricidae; Tortricinae; Choristoneura.
OX NCBI_TaxID=7141;
[1]
RRN SEQUENCE FROM N.A.
RRP Zheng X., Zheng S., Cheng X., Ladd T., Krell P.J., Arif B.,
RA Retnakaran A., Feng O.;
RA "A mole-associated chitinase cDNA from the spruce budworm,
RT Choristoneura fumiferana";
RRL Submitted (APR-2002) to the ENBL/GenBank/DBJ databases.
DR EMBL; AY098731; AAA43792.1;
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008061; F:chitin binding; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0006030; P:chitin metabolism; IEA.
DR InterPro; IPR002557; Chitin bind PerA.
DR InterPro; IPR001223; Glyco_hydro_18.
DR InterPro; IPR001579; Glyco_hydro_18As.
DR Pfam; PF01607; CBM_14; 1.
DR Pfam; PF00704; Glyco_hydro_18; 1.
DR ProDom; PD000471; Glyco_hydro_18; 1.
DR SMART; SM00494; ChtBD2; 1.
DR SMART; SM00636; Glyco 18; 1.

```

DR PROSITE; PS01095; CHITINASE_18; 1.
SQ SEQUENCE 557 AA; 62227 MW; 2CF7827D6A294AD5 CRC64;

Query Match      27.3%; Score 821.5; DB 5; Length 557;
Best Local Similarity 34.7%; Pred. No. 2.2e-43;
Matches 193; Conservative 79; Mismatches 207; Indels 77; Gaps 16;

QY 10 SKNPMRIVCVGWGSVYHK-VDPYTTIEDIDPKCTHLMYGPAPKIDBYKYTIQVDFYQDD 68
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 20 SEGRIIVYCFSNWVYRPGVGRYGVIEDIPVMCTHIIYSFGIVGTENTHELVLDPELDE 79
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 69 NHNSWKRQYVERFNRLKKNPELTMTISLGGWYEGSEKYSDMAANPTYRQCFQCSVLDEL 128
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 80 -----BKNGFRNFTSUKANHPDIKFWVAVGGWAEGSKSYSHWVAQSSRWAFVYKSVVDLF 134
QY 129 QEYKFDGLDLIDWEYPGSR-LGNPKIDKQNYLALVRELKDAF--EPHGYLITAAVSPGKOK 185
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 135 HKNYFDGLDLIDWEYPGAADRGGSFSKDRFLYLVLQELRRAFIRAGKGWELTAAVPLANFR 194
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 186 IDRAYDIKELNLFDMWNVMTYDYGWGNFYGHNAPLYKRPDETDELHTFYFNVTMTHY 245
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 195 LMEGYHVPDLCELDIAHYMSVDLRGNWAGFADVHSPLYKRRPHD-QWAYEKLNVNDGLNL 253
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 246 YLNGGATRDKLWGVGPYGRANSIED-----RSKLKLGDPAGKWSPPGFTSGEE 294
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 254 WBEKGCPSKNLVGVIEFYGRSFTLSAGNNYGLGTTINKEAGGGDPAPYTNATGF----- 308
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 295 GVLSYTELQQLFOKEB--WHIQVDEYYPNPGYNDKIWGVYDDLASISCKLAPFKELGVS 352
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 309 --WAYYEICTEVDKDSGHTKKWDEAGKCPYAKGTQWGVYEDERSVEIKMNWIKKGYL 366
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 353 GVMVWSELENDDFKGHGCGKPNLLKVNHNINGDEKNSFECILGFSVTTPTPTPTPTPTPT- 411
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 367 GAMTWAVDMDDFRGLCGDTNPLKLLHKHS-----SYTVPPPTTGNTTPTTP 413
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 412 -----TTPTTSPPTPTPTTPS--PTPTPTTSPPTPTPTPTPTPTPTPTPT 450
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 414 EWARPSTGANPSEGAPIPTTIAPKPAVXPVPTVKPSKPTTNA--APTITKAEAEV 471
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 451 PTTPTPAPTTSPTSPPTTTEHTSBTPKYTYTVVDGHLIKCYKEGDIPIPTNTHKLYLVCFVN 510
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 472 PKPE-EPAPVVPBIPDVREQPTDNE-----VDDHRVCDNDEYIPDKKCDKYWRC--VN 523
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 511 GGWVHHMPCPGGTIW 526
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 524 GEGVQ--FTCQPGTVF 537
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

RESULT 14

Q9GR93	PRELIMINARY;	PRT;	543 AA.
ID	Q9GR93		
AC	Q9GR93;		
DT	01-MAR-2001 (T-EMBLrel. 16, Created)		
DT	01-MAR-2001 (T-EMBLrel. 16, Last sequence update)		
DT	01-OCT-2003 (T-EMBLrel. 25, Last annotation update)		
DE	Chitinase precursor [EC 3.2.1.14].		
GN	CHIB.		
OS	Bombyx mori (Silk moth).		
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;		
OC	Nemoptera; Endopterygota; Lepidoptera; Glossata; Bombycoidea;		
OC	Bombycidae; Bombyx.		
OX	NCBI_TaxID=7091;		
OX	[1]		
RP	SEQUENCE FROM N.A.		
RP	STRAIN=Kinshu x Showa; TISSUE=Integument;		
RC	Abdel-Banat B.M., Koga D.;		
RT	"Molecular cloning of Bombyx mori chitinase cDNA: a unique insert of 9		
RT	base pairs reduced the apparent molecular mass of the encoded		
RT	protein.";		
RL	Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.		
RL	EMBL; AB052914; BAB20017.1; -.		
DR	GO; GO:0005576; C:extracellular; IEA.		
DR	GO; GO:0008061; F:chitin binding; IEA.		

DR GO:0008843; F:endochitinase activity; IEA.
 DR GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
 DR GO:0005975; P:carbohydrate metabolism; IEA.
 DR GO:0006030; P:chitin metabolism; IEA.
 DR InterPro: IPR002557; Chitin bind PerA.
 DR InterPro: IPR001223; Glyco_hydro_18.
 DR InterPro: IPR001579; Glyco_hydro_18AS.
 DR Pfam: PF01607; CEM_14; 1.
 DR Pfam: PF00704; Glyco_hydro_18; 1.
 DR ProDom: PD000471; Glyco_hydro_18; 1.
 DR SMART: SM00494; ChtBD2; 1.
 DR SMART: SM00636; Glyco_18; 1.
 DR PROSITE: PS01095; CHITINASE_18; 1.
 DR GlycoSite: Hydrolase; Signal.
 KW SIGNAL 1 20 POTENTIAL.
 FT CHAIN 21 543 CHITINASE.
 SQ SEQUENCE 543 AA; 60971 MW; C36C71E3B84DF88 CRC64;
 Query Match 27.2%; Score 819; DB 5; Length 543;
 Best Local Similarity 36.6%; Pred. No. 3e-43;
 Matches 200; Conservative 72; Mismatches 203; Indels 72; Gaps 18;
 QY 10 SKNPMRIVCYVGTWSVYHK-VDPYTIEDIDPKCTHLMYGFADKIDYKTIQVDFDPYQDD 68
 DB 20 SDSRARIVCYFSNVAWYRPGVGRYGIEDIPVDLCTHLYISFVIGTEKSSSEVLIDPELD- 78
 QY 69 NHNSWEKRGYRFFNNLRKNLPETMTISLGWYEGSEKYSMDAANPYRQOFTQSVLDLFL 128
 DB 79 ----VDKSGPRNFTSLRKHDPVFMVAVGWAEGSGKYSHWAAQKSTRMSFIRSVDFL 134
 QY 129 QEYKFDGLDLWEYFGSR-LGNPKIDKQNYLALVRELKDAF--EPHGYLITAAVSPGKDK 185
 DB 135 KKYDFDGLDLWEYFGAADRGGSDKDFLYFVQELKEAFIRAGRWELTAAPLANFR 194
 QY 186 IDRAYDIKELNKLFDMMNVTYDYGWENFYGHNAPLYKRPDETDELHLYFNVTMTHY 245
 DB 195 LMBGYHVPBELCOELDAIHVMSYDLRGWAGFADVHSPLYKRPD-QWAYEKLNVNDGLNL 253
 QY 246 YLNNGATRDKLVMGVPFYGRAWISIED-----RSKLKLGDPAGKMSPPGFISGEE 294
 DB 254 WEEKGCPNKLVIIGFVGRSFTLSAGNNYGLGTVINKEAGGDPAPYNTATGF----- 308
 QY 295 GVLVSIELCOLFOKE--EWHIOYDEVYNAPYGVNDKIWGVYDDLASISCKLAFKELGVS 352
 DB 309 --WAYEICTEVDADGSGTKWDFKCPYAKGTQWVGVEDPRSVELKMWIKKGYL 366
 QY 353 GVMVWSLENDDFKGGCKPNLKNVHNMINGDEKNSFECILGSPSTTTPTTPTTPTTPTT 412
 DB 367 GANTWALDMDDFKGLCGSENLPLKLRHMS-----THTVPPARTGHTTPTP 413
 QY 413 TPTTPTTPTTPTT-----TPSPPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTT 468
 DB 414 EWARP-PSPTSDPSEGDPIPTTTTIVKPTTRTARPTT-----TTTKVPHGTTTE 463
 QY 469 E-----HTSETPKYTYVDGHLIKCYKEGD-IPHPTNIHKYLVCEFGVNGGWWHIMP 519
 DB 464 EDFDINVRPEVELPT-ENEVDNADV-CNSEDDYVDPKCKECSKYWRC--VNGEGVQ--FS 517
 QY 520 CPGPTW 526
 DB 518 CQPGTIF 524
 RESULT 15
 Q9GV05 PRELIMINARY; PRT; 543 AA.
 AC Q9GV05;
 DT 01-WAR-2001 (TrEMBLrel. 16, Created)
 DT 01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Chitinase precursor (EC 3.2.1.14).
 OS CHI.
 OS Bombyx mori (Silk moth).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Bombycoidea;
 OC Bombycidae; Bombyx.
 OX NCBI_TaxID=7091;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Kinshu X Showa hybrid; TISSUE=Integument;
 RX MEDLINE=21124800; PubMed=11222960;
 RA Abdel-Banat B.M.A.; Koga D.;
 RT "A genomic clone for a chitinase gene from the silkworm, Bombyx mori:
 RL structural organization identifies functional motifs.";
 RL Insect Biochem. Mol. Biol. 31:497-508(2001).
 DR EMBL; AB048355; BAB13481.1; .
 DR GO:0005576; C:extracellular; IEA.
 DR GO:0008061; P:chitin binding; IEA.
 DR GO:0008843; F:endochitinase activity; IEA.
 DR GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
 DR GO:0005975; P:carbohydrate metabolism; IEA.
 DR GO:0006030; P:chitin metabolism; IEA.
 DR InterPro: IPR002557; Chitin bind PerA.
 DR InterPro: IPR001223; Glyco_hydro_18.
 DR InterPro: IPR001579; Glyco_hydro_18AS.
 DR Pfam: PF01607; CEM_14; 1.
 DR ProDom: PD000471; Glyco_hydro_18; 1.
 DR SMART: SM00494; ChtBD2; 1.
 DR SMART: SM00636; Glyco_18; 1.
 DR PROSITE: PS01095; CHITINASE_18; 1.
 KW Glycosidase; Hydrolase; Signal.
 FT SIGNAL 1 20 POTENTIAL.
 FT CHAIN 21 543 CHITINASE.
 SQ SEQUENCE 543 AA; 60982 MW; DE29675D83AEC2EF CRC64;
 Query Match 27.2%; Score 819; DB 5; Length 543;
 Best Local Similarity 36.6%; Pred. No. 3e-43;
 Matches 200; Conservative 72; Mismatches 203; Indels 72; Gaps 18;
 QY 10 SKNPMRIVCYVGTWSVYHK-VDPYTIEDIDPKCTHLMYGFADKIDYKTIQVDFDPYQDD 68
 DB 20 SDSRARIVCYFSNVAWYRPGVGRYGIEDIPVDLCTHLYISFVIGTEKSSSEVLIDPELD- 78
 QY 69 NHNSWEKRGYRFFNNLRKNLPETMTISLGWYEGSEKYSMDAANPYRQOFTQSVLDLFL 128
 DB 79 ----VDKSGPRNFTSLRKHDPVFMVAVGWAEGSGKYSHWAAQKSTRMSFIRSVDFL 134
 QY 129 QEYKFDGLDLWEYFGSR-LGNPKIDKQNYLALVRELKDAF--EPHGYLITAAVSPGKDK 185
 DB 135 KKYDFDGLDLWEYFGAADRGGSDKDFLYFVQELKEAFIRAGRWELTAAPLANFR 194
 QY 186 IDRAYDIKELNKLFDMMNVTYDYGWENFYGHNAPLYKRPDETDELHLYFNVTMTHY 245
 DB 195 LMBGYHVPBELCOELDAIHVMSYDLRGWAGFADVHSPLYKRPD-QWAYEKLNVNDGLNL 253
 QY 246 YLNNGATRDKLVMGVPFYGRAWISIED-----RSKLKLGDPAGKMSPPGFISGEE 294
 DB 254 WEEKGCPNKLVIIGFVGRSFTLSAGNNYGLGTVINKEAGGDPAPYNTATGF----- 308
 QY 295 GVLVSIELCOLFOKE--EWHIOYDEVYNAPYGVNDKIWGVYDDLASISCKLAFKELGVS 352
 DB 309 --WAYEICTEVDADGSGTKWDFKCPYAKGTQWVGVEDPRSVELKMWIKKGYL 366
 QY 353 GVMVWSLENDDFKGGCKPNLKNVHNMINGDEKNSFECILGSPSTTTPTTPTTPTTPTT 412
 DB 367 GANTWALDMDDFKGLCGSENLPLKLRHMS-----THTVPPARTGHTTPTP 413
 QY 413 TPTTPTTPTTPTT-----TPSPPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTT 468
 DB 414 EWARP-PSPTSDPSEGDPIPTTTTIVKPTTRTARPTT-----TTTKVPHGTTTE 463
 QY 469 E-----HTSETPKYTYVDGHLIKCYKEGD-IPHPTNIHKYLVCEFGVNGGWWHIMP 519
 DB 464 EDFDINVRPEVELPT-ENEVDNADV-CNSEDDYVDPKCKECSKYWRC--VNGEGVQ--FS 517

QY 520 CQPGTIW 526
| | | | |
Db 518 CQPGTIF 524

Search completed: March 22, 2004, 06:59:27
Job time : 108.855 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 22, 2004, 06:31:13 ; Search time 20.5581 Seconds
(without alignments)
1357.597 Million cell updates/sec

Title: US-09-662-293-21
Perfect score: 3014
Sequence: 1 SIKEDHNDYKNPWIRVCYV.....IMPCPPTGTCQKLTICGE 536

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	834	27.7	554	1 CHIT_MANSE	P36362 manduca sex
2	738	24.5	466	1 CHIT_HUMAN	Q12331 homo sapien
3	727.5	24.1	473	1 CHIA_MOUSE	Q91xa9 mus musculu
4	723	24.0	508	1 CHIL_DROME	Q9w5u3 drosophila
5	708.5	23.5	476	1 CHIA_HUMAN	Q9b2p6 homo sapien
6	705.5	23.4	617	1 CHIT_CAEEL	Q11174 caenorhabdi
7	694.5	23.0	527	1 OGP_PIG	Q28990 sus scrofa
8	682.5	22.6	381	1 OGP_SHEEP	Q28542 ovis aries
9	680	22.6	381	1 C3L1_MOUSE	Q61362 mus musculu
10	680	22.6	721	1 OGP_MOUSE	Q62010 mus musculu
11	677.5	22.5	671	1 OGP_MESAU	Q60557 mesocricetu
12	673	22.3	537	1 OGP_BOVIN	Q28042 bos taurus
13	667.5	22.1	678	1 OGP_HUMAN	Q12889 homo sapien
14	660	21.9	383	1 C3L1_HUMAN	P36222 homo sapien
15	654	21.7	623	1 OGP_PAPAN	P16718 papio anubi
16	630	20.9	390	1 C3L2_HUMAN	Q15782 homo sapien
17	611.5	20.3	396	1 CHIT_MOUSE	Q3d7d1 mus musculu
18	604.5	20.1	504	1 CHIT_BRUMA	P29030 brugia mala
19	576	19.1	458	1 CH13_DROME	Q9w5u2 drosophila
20	561	18.6	699	1 CH11_BACCI	P20533 bacillus ci
21	409.5	13.6	423	1 CH11_APHAL	P32470 aphanoeladi
22	407.5	13.5	563	1 CHIA_SERVA	P07254 serratia ma
23	402.5	13.4	423	1 CH14_TRIHA	P48827 trichoderma
24	384	12.7	820	1 CHIA_ALTISO	P32823 altomonas
25	377.5	12.5	550	1 CHIT_NPVOP	Q10363 orgyia pseu
26	360.5	12.0	551	1 CHIT_NPVAC	P41684 autographa
27	353	11.7	499	1 CHIB_SERVA	P11757 serratia ma
28	341	11.3	619	1 CHIT_STRLI	P36909 streptomyce
29	339.5	11.3	427	1 CH11_COCOPO	P54196 coccidioid
30	326	10.8	610	1 CHIT_STRPL	P11220 streptomyce
31	280	9.3	1046	1 CHID_VIBFU	P96156 vibrio furn
32	266.5	8.8	474	1 VTP3_TTVIV	P19275 thermoprote
33	259	8.6	5179	1 MUC2_HUMAN	Q02817 homo sapien

34	247	8.2	1513	1 MUC1_RAT	Q62635 rattus norv
35	244	8.1	662	1 MUC1_XENLA	Q05049 xenopus lae
36	238	7.9	279	1 Y091_NPVOP	O10341 orgyia pseu
37	230	7.6	400	1 MUA1_XENLA	P10667 xenopus lae
38	227.5	7.5	1331	1 MANB_CALSA	P22533 caldocellum
39	221	7.3	267	1 EXTN_MAIZE	P14918 zea mays (m
40	217.5	7.2	544	1 GP10_DICDI	Q05885 dictyosteli
41	217.5	7.2	1161	1 DAN4_YEAST	P47179 saccharomyc
42	215.5	7.1	705	1 GUN6_DICDI	P22699 dictyosteli
43	215.5	7.1	1146	1 KTXA_KLULA	P09805 kluyveromyc
44	208.5	6.9	283	1 EXTN_SORBI	P24152 sorghum bic
45	207	6.9	307	1 SGS3_DROME	P02840 drosophila

ALIGNMENTS

RESULT 1

ID	CHIT_MANSE	STANDARD;	PRT;	554 AA.
DT	01-JUN-1994 (Rel. 29, Created)			
DT	01-JUN-1994 (Rel. 29, Last sequence update)			
DT	15-MAR-2004 (Rel. 43, Last annotation update)			
DE	Endochitinase precursor (EC 3.2.1.14).			
OS	Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).			
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;			
OC	Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Sphingioidea;			
OC	Sphingidae; Sphinginae; Manduca.			
OX	NCBI_TaxID=7130;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=9335793; PubMed=8353525;			
RA	Kramer K.J., Corpuz L., Choi H.K., Muthukrishnan S.;			
RT	"Sequence of a cDNA and expression of the gene encoding epidermal and			
RT	gut chitinases of Manduca sexta."			
RL	Insect Biochem. Mol. Biol. 23:691-701(1993).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=97215580; PubMed=9061927;			
RA	Choi H.K., Choi K.H., Kramer K.J., Muthukrishnan S.;			
RT	"Isolation and characterization of a genomic clone for the gene of an			
RT	insect molting enzyme, chitinase."			
RL	Insect Biochem. Mol. Biol. 27:37-47(1997).			
CC	-!- FUNCTION: Digest chitin in the exoskeleton during the molting			
CC	process.			
CC	-!- CATALYTIC ACTIVITY: Hydrolysis of the 1,4-beta-linkages of N-			
CC	acetyl-D-glucosamine polymers of chitin.			
CC	-!- SUBCELLULAR LOCATION: Secreted.			
CC	-!- TISSUE SPECIFICITY: Epidermis and gut.			
CC	-!- DEVELOPMENTAL STAGE: High levels seen in the epidermis on day 0,			
CC	but rapidly disappears and is undetected on days 1-4 of fifth			
CC	instar. It reappears on day 5 and peaks on day 7 after which a			
CC	rapid decline is seen. In the gut is detected on day 6 with lower			
CC	levels seen on days 0, 7 and 8.			
CC	-!- SIMILARITY: Belongs to chitinase class II (family 18 of glycosyl			
CC	hydrolases).			
CC	-!- SIMILARITY: Contains 1 chitin-binding type-2 domain.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
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CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; U02270; AAC04924.1; -			
DR	EMBL; L49234; AAC53952.1; -			
DR	PIR; A56596; A56596			
DR	InterPro; IPR002557; Chitin_bind_Pera.			
DR	InterPro; IPR001223; Glyco_Hydro_18.			
DR	InterPro; IPR001579; Glyco_Hydro_18AS.			

[illegible]

RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahay J., Helton E., Kettanan M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A.C., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP SEQUENCE OF 2-473 FROM N.A.
RC TISSUE-Skin; Harris S.C., Williamson M.K.;
RA Price P.A., Harris S.C., Williamson M.K.;
RT "YNI, a putative mouse chitinase.";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Degrades chitin and chitotriose. May participate in the
CC defense against nematodes and other pathogens.
CC -!- CATALYTIC ACTIVITY: Hydrolysis of the 1,4-beta-linkages of N-
CC acetyl-D-glucosamine polymers of chitin.
CC -!- SUBCELLULAR LOCATION: Secreted (Probable).
CC -!- TISSUE SPECIFICITY: Highly expressed in submaxillary gland, and
CC stomach. Expressed at lower levels in lung.
CC -!- SIMILARITY: Belongs to chitinase class II (family 18 of glycosyl
CC hydrolases).
CC -!- SIMILARITY: Contains 1 chitin-binding type-2 domain.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF290003; AAG60018.1; -;
DR EMBL; AK008633; BAB25795.1; -;
DR EMBL; BC011134; AAH1134.1; ALT INIT.
DR EMBL; BC034548; AAH34548.1; ALT INIT.
DR EMBL; AF154571; AAF31644.1; -;
DR MGD; MGI:1932052; Chia.
DR GO; GO:0004568; F:chitinase activity; IDA.
DR GO; GO:0006032; P:chitin catabolism; IDA.
DR InterPro; IPR002557; Chitin_bind_Pera.
DR InterPro; IPR001223; Glyco_hydro_18.
DR InterPro; IPR001579; Glyco_hydro_18AS.
DR Pfam; PF01607; CEM_14; 1.
DR Pfam; PF00704; Glyco_hydro_18; 1.
DR ProDom; PD000471; Glyco_hydro_18; 1.
DR SMART; SM00494; ChtB2; 1.
DR SMART; SM00636; Glyco_18; 1.
DR PROSITE; PS50940; CHIT_BIND_II; 1.
DR PROSITE; PS01095; CHITINASE_18; 1.
DR Carbohydrate metabolism; Chitin degradation;
KW Polysaccharide degradation; Hydrolase; Glycosidase; Chitin-binding;
KW Signal.
FT SIGNAL 1 21
FT CHAIN 22 473 ACIDIC MAMMALIAN CHITINASE.
FT DOMAIN 424 473 CHITIN-BINDING TYPE-2.
FT ACT_SITE 140 140 BY SIMILARITY.
FT DISULFID 26 51 BY SIMILARITY.
FT DISULFID 307 372 BY SIMILARITY.
FT CONFLICT 293 P -> A (IN REF. 1).
SQ SEQUENCE 473 AA; 52003 MW; 333C874477476695 CRC64;
Query Match 24.1%; Score 727.5; DB 1; Length 473;
Best Local Similarity 37.0%; Pred. No. 6.7e-33;
Matches 154; Conservative 69; Mismatches 144; Indels 49; Gaps 11;
QY 16 IVCYVGTWSVYHK-VDPTIEDIPKCTHLMYGFADKIDEXYKIQVDFPDQDDNHNWS- 73
DB 24 LICFTFNWQAQYRPLGSGFKPDDINPCLCITHLIYAFAGMGNNEITT-----IENW 72

QY 74 EKRGYERFNNLRKLNPELTMTISLGGWYEGSEKYSDMAANPTVROQFIQSVLDFLOEYKF 133
DB 73 DVTLYKAFNDLKNRNSKLTLLAIGWNVTGAPFTTWSTQNRQTFITSVIKFLRQYGF 132
QY 134 DGLDLWEYPSGRSLGNPKIDKQNYLALVELKDAFEPHG-----YLTAAVSPGKDKI 186
DB 133 DGLDLWEYPSGR-GSPPODKHLFTVLKEMREAFQEAIESNRPLMVTAAVAGGISNI 191
QY 187 DRAYDIKELNKLFDWNNVTYDHYGWNFYGHNAPLYKRPDETDLHTYFNNVYTHYY 246
DB 192 QAGYEIPFLSKYLDFTHVNTYDLHGSWEGYTGNSLYKPYTETGS-NAYLVNDYVNNYW 250
QY 247 LNNGATEDKLVMGVFPVYGRAWSIEDRSKLKIDPAKGMSPPGFISGEEGVLSIELCOLF 306
DB 251 KXNGAPAKKLIVGFPYGHFTILRNPSDNGIGAPTSGDGPAGYTRQAGFWAYEICTFL 310
QY 307 QK---BEWHIQYDEYNNAPYGVNDKIKWGVYDDIASISCKLAFKELGLVSGVMVWSLEND 363
DB 311 RSGATEVW----DASQEVFVAYKANEWLGVNDIKSFVKAQWLKQNNFGGAMTWAIDLD 366
QY 364 FKQ-HCG-----PKNPLLNKVNHNMGDEKNSFECILGPSTTTPTTTPTTTPTTT 414
DB 367 FTGSGFCDQKGFPLTSLNKA-----LGISTEGCTAPDVPSEPTTP 407
RESULT 4
CH11 DROME
ID CH11 DROME STANDARD; PRT; 508 AA.
AC Q9W5J3; O17420;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Probable chitinase 1 (EC 3.2.1.14).
GN CHT1 OR CG17682.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RA MEDLINE=22426071; PubMed=12537574;
RA Hoskins R.A., Smith C.D., Carlson J.W., Carvalho A.B., Halpern A.,
RA Kaminker J.C., Kennedy C., Mungall C.J., Sullivan B.A., Sutton G.G.,
RA Yasuhara J.S., Wakimoto B.T., Myers E.W., Celniker S.E., Rubin G.M.,
RA Karpen G.H.;
RT "Heterochromatic sequences in a Drosophila whole-genome shotgun
RT assembly.";
RL Genome Biol. 3:RESEARCH0085.1-RESEARCH0085.16(2002).
RN [2]
RP SEQUENCE OF 151-263 FROM N.A.
RC STRAIN=Canton-S;
RA MEDLINE=98324849; PubMed=9662472;
RA de la Vega H., Specht C.A., Liu Y., Robbins P.W.;
RT "Chitinases are a multi-gene family in Aedes, Anopheles and
RT Drosophila.";
RL Insect Mol. Biol. 7:233-239(1998).
CC -!- CATALYTIC ACTIVITY: Hydrolysis of the 1,4-beta-linkages of N-
CC acetyl-D-glucosamine polymers of chitin.
CC -!- SIMILARITY: Belongs to chitinase class II (family 18 of glycosyl
CC hydrolases).
CC
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CC
CC EMBL; AF026500; AAB81858.1; -;
DR EMBL; FBgn0022703; Chti.


```
DR InterPro; IPR001223; Glyco_hydro_18.
DR InterPro; IPR001579; Glyco_hydro_18AS.
DR Pfam; PF00704; Glyco_hydro_18; 2.
DR ProDom; PD000471; Glyco_hydro_18; 2.
DR SMART; SM00836; Glyco_18; 1.
DR PROSITE; PS01095; CHITINASE_18; 1.
KW Hydrolase; Glycosidase; Chitin degradation; Multigene family.
FT ACT_SITE 264 264 PROTON DONOR (BY SIMILARITY).
SQ SEQUENCE 508 AA; 57751 MW; 26CA23802EFD97 CRC64;

Query Match          274.0%; Score 723; DB 1; Length 508;
Best Local Similarity 39.8%; Pred. No. 1.3e-32;
Matches 144; Conservative 71; Mismatches 121; Indels 26; Gaps 9;

QY 15 RIVCYGTWSVYHK-VDPYTIEDIDPEKCTHLMYGAIDYKYTIQVDPQDDNNHNSW 73
Db 143 KIICYFTNWAYRQGGGKFLPDISDLCTHIYGFVLSRDNLTIQ-----PHDSW 194
QY 74 --EKGYERFNNLRKNPELTTWISLGGWYEGS-EKYSDMAANPTVROFTQSVLDLFLQ 129
Db 195 ADLNKPYEIVAYRKGAQVT--VAIGWNDSAGDKYSLVRNPEARSRFRINRLDFTIE 252
QY 130 EYKFDGLDLDEWYP-----GSRLEGNPKIDKQNTYLAIVRELKDAFEPHGVLITAAVSPGKD 184
Db 253 EYNFDGLDLDEWYPCWQVDCCKGTAE-EKIGESALVRELFPYAFQPRGLILSNAVSPNKK 311
QY 185 KIDRAYDIKELKLFDMNNVMTYDYGWENFYGHNAPLYKRPDETDLHTYFNVNNTWH 244
Db 312 VIDAGYEVAELSHVFSWISWVAYDYGQWDKKTGHVAPWYSHDEGT----ANFNANFSWN 367
QY 245 YLLNGATRLKLVGPPFYGRANSIEDRSKILGDPAGKMSPPGFTSGEGVLSYIELCQ 304
Db 368 YWISMGADRKLKLVGPIYQSGFSLAETTKHQLNAPTYGGGEAGEATRAGFLAYVEICL 427
QY 305 LFQKEEHIQYDEYN-APGYNDKTVGWGVDDLASISKLAFKELGVSGVWVMSLEND 363
Db 428 KIRHRNVRVDTKGRIGPPAYHGQDQVSPDDVFNIRHKSEYIKAMGLGAMINWALDLD 487
QY 364 FK 365
Db 488 FK 489

RESULT 5
CHIA_HUMAN STANDARD; PRT; 476 AA.
AC Q9BZP6; Q86UD8; Q9ULY3; Q9ULY4;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Acidic mammalian chitinase precursor (EC 3.2.1.14) (AMCase)
DE (TSA1902).
GN CHIA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 2 AND 3).
RC TISSUE=Lung;
RX MEDLINE=20018184; PubMed=10548734;
RA Saito A., Ozaki K., Fujiwara T., Nakamura Y., Tanigami A.;
RT "Isolation and mapping of a human lung-specific gene, TSA1902,
RT encoding a novel chitinase family member.";
RL Gene 239:325-331(1999).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1), FUNCTION, AND TISSUE SPECIFICITY.
RC TISSUE=Lung, and Stomach.
RX MEDLINE=21125893; PubMed=11085997;
RA Boot R.G., Blommaert E.F.C., Swart B., Ghauharali-van der Vlugt K.,
RA Bijl N., Moe C., Place A., Aerts J.M.F.G.;
RT "Identification of a novel acidic mammalian chitinase distinct from
RT chitotriosidase."
```

```
RL J. Biol. Chem. 276:6770-6778 (2001).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.W., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield J.S.N., Krzywinski M.I., Skalska U., Marra M.A.;
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC -!- FUNCTION: Degrades chitin and chitotriose. May participate in the
CC defense against nematodes and other pathogens.
CC -!- CATALYTIC ACTIVITY: Hydrolysis of the 1,4-beta-linkages of N-
CC acetyl-D-glucosamine polymers of chitin.
CC -!- SUBCELLULAR LOCATION: Secreted (Probable). Isoform 2 and isoform 3
CC lack the signal sequence and are cytoplasmic.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=1;
CC IsoId=Q9BZP6-1; Sequence=Displayed;
CC Name=2; Synonyms=TSAL902-L; Sequence=VSP_008635;
CC IsoId=Q9BZP6-2; Sequence=VSP_008635;
CC Name=3; Synonyms=TSAL902-S;
CC IsoId=Q9BZP6-3; Sequence=VSP_008634;
CC -!- TISSUE SPECIFICITY: Highly expressed in stomach. Detected at lower
CC levels in lung.
CC -!- SIMILARITY: Belongs to chitinase class II (family 18 of glycosyl
CC hydrolases).
CC -!- SIMILARITY: Contains 1 chitin-binding type-2 domain.
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CC EMBL; AB025008; BAAS6980.1; -
CC EMBL; AB025009; BAAS6981.1; -
CC EMBL; AF290004; AAG60019.1; -
CC EMBL; BC047336; AAH47336.1; ALT_INIT.
CC MIM; 606080; -
CC GO; GO:0005737; C:cytoplasm; NAS.
CC GO; GO:0004568; F:chitinase activity; NAS.
CC GO; GO:0006030; F:chitin metabolism; NAS.
CC InterPro; IPR002557; Chitin bind PerA.
CC InterPro; IPR001223; Glyco_hydro_18.
CC InterPro; IPR001579; Glyco_hydro_18AS.
CC Pfam; PF01607; CBM_14; 1.
CC ProDom; PD000471; Glyco_hydro_18; 1.
CC SMART; SM00636; Glyco_18; 1.
CC SMART; SM00494; ChitBD2; 1.
CC PROSITE; PS05940; CHIT_BIND_II; 1.
CC PROSITE; PS01095; CHITINASE_18; 1.
KW Carbohydrate metabolism; Chitin degradation;
KW Polysaccharide degradation; Hydrolase; Glycosidase; Chitin-binding;
```

KW Signal; Alternative splicing.
FT SIGNAL 1 21
FT CHAIN 22 476
FT DOMAIN 427 476
FT DOMAIN 415 420
FT ACT_SITE 140 140
FT DISULFID 26 51
FT DISULFID 307 372
FT VARSPLIC 1 161
FT VARSPLIC 1 108
FT CONFLICT 339 339
FT CONFLICT 432 432
FT CONFLICT 432 432
SQ SEQUENCE 476 AA; 52271 MW; 92B27BAD2F7EB4CC CRC64;

Query Match 23.5%; Score 708.5; DB 1; Length 476;
Best Local Similarity 35.9%; Pred. No. 7.2e-32;
Matches 149; Conservative 75; Mismatches 154; Indels 37; Gaps 10;

QY 15 RIVCVGTWSTYHK-VDPYTIEDIDPFKCHLMYGFADKIDYKTIQVDFPYQDDNHNWSW 73
DB 23 QLTCTFNWQYRGLGRFPDNDIDPCLCHLLIYAFAGRNNEITT-----IEW 71

QY 74 -EKGYERFNNLRKLNPELTMTISLGGWYEGSEKYSDMAANPTYRQOFIOSVLDFLOEYK 132
DB 72 NDVTLYQAFGLKKNKSQLKTLAIGGNFGTAPFTAWSTPENRQTFITSVIKFLRQYE 131

QY 133 FDGLDWEYVPGSRGLGNPKIDKQNYLALVRELKDAPEPHG-----YLLTAVSPGKDK 185
DB 132 FDGLDWEYVPGSR-GSPQDQKHLFTVLQEMREAFQEAQKQINPKLPMATAAAGISN 190

QY 186 IDRAYDIKELNKLFDWNNVTYDHGWNFYGHNAPLYKRPDETDELHTYNNVTMTHY 245
DB 191 IQSGYEIPQLSQYLDYHVMTYDILHSGWEGTGENSPLYKYPTDTGS-NAYLNVYVMNY 249

QY 246 YLNNGATRDVLVGVPPFYGRAWS-EDRSKLGKLGDPAGKMSPPGPGISGEGVLSYIELCOL 305
DB 250 WKONGAPAEKLIIVFPYGHNFILSNFNTGIGAPTSGAGPAGPYAKESGIWAYYEIC-T 308

QY 306 PQKEEWHIQDYENYAPYNDKIVGYDDIASISCKLAFELKELGVSGVMVNSLENDDFK 365
DB 309 FLKNGATOGWADAPQEVYAYQGVNMGVYDNKISFDIKAQWLKHNKFGAMVWVWVWVWV 368

QY 366 G-HGCP-KNPLLNKVNHNMGDEKNSFECILGPSTPTPTPTPTPTPTPTPTPTPTPTPS 418
DB 369 GTFCNQGRFPLI-----STLKKALGLOSASCTAPAQPIEPTAAPS 411

RESULT 6
CHIT CAEEL
ID CHIT CAEEL STANDARD; PRT; 617 AA.
AC Q11174; O17321;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Probable endochitinase (EC 3.2.1.14).
GN CHT-1 OR C04F6.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Nham M.;
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 62-178 FROM N.A.
RX MEDLINE=98324849; PubMed=9662472;
RA de la Vega H.; Specht C.A.; Liu Y.; Robbins P.W.;
RT "Chitinases are a multi-gene family in Aedes, Anopheles and Drosophila."

Insect Mol. Biol. 7:233-239(1998).
-I- CATALYTIC ACTIVITY: Hydrolysis of the 1,4-beta-linkages of N-acetyl-D-glucosamine polymers of chitin.
-I- SIMILARITY: Belongs to chitinase class II (family 18 of glycosyl hydrolases).
-I- SIMILARITY: Contains 2 chitin-binding type-2 domains.

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EMBL; U42835; AAB83586.1; -
EMBL; AF026152; AAB81847.1; -
PIR; T15408; T15408.
PIR; T37249; T37249.
Wormpep; C04F6.3; C039323.
InterPro; IPR002557; Chitin bind_Pera.
InterPro; IPR001223; Glyco_hydro_18.
InterPro; IPR001579; Glyco_hydro_18AS.
Pfam; PF01607; CBM 14; 2.
Pfam; PF00704; Glyco_hydro_18; 1.
ProDom; PD000471; Glyco_hydro_18; 1.
SMART; SM00494; ChitED2; 2.
SMART; SM00636; Glyco 18; 1.
PROSITE; PS00940; CHIT BIND II; 2.
PROSITE; PS01095; CHITINASE 18; 1.
KW Hydrolyase; Glycosidase; Chitin degradation; Chitin-binding; Repeat.
FT DOMAIN 478 534
FT ACT_SITE 563 617
FT ACT_SITE 179 179
FT DOMAIN 435 478
FT DOMAIN 138 138
FT CONFLICT 153 165
FT CONFLICT 176 176
SQ SEQUENCE 617 AA; 66857 MW; DDA1D2AAAC0ES4DA CRC64;

Query Match 23.4%; Score 705.5; DB 1; Length 617;
Best Local Similarity 30.2%; Pred. No. 1.4e-31;
Matches 178; Conservative 90; Mismatches 210; Indels 111; Gaps 19;

QY 18 CVVGTWSTYHK-VDPYTIEDIDPFKCHLMYGFADKIDYKTIQVDFPYQDDNHNSEWR 76
DB 57 CHTNWAQYRQRAKEVPEDEYTPGLCTHLLFAFGMNA-DYTVRAYDP--ADLPNDWAGE 113

QY 77 G-YERFNNLRKLNPELTMTISLGGWYEGSEKYSDMAANPTYRQOFIOSVLDFLOEYKFG 135
DB 114 GWYRVNKLKVTDTQLKTLSPGWSFGTALFQGMASASAKRVFTDSAITFVWTGFDG 173

QY 136 LLDWEYVPGSRGLGNPKIDKQNYLALVRELKDAPEPHG-----YLLTAVSPGKDKIDR 188
DB 174 IDIDWEYVPG-----ATDMANYVALVKELKAAACESEAGSTGKDRLLVTAAGAATIDA 228

QY 189 AYDIKELNKLFDWNNVTYDHGWNFYGHNAPLYKRPDETDELHTYNNVTMTHYLN 248
DB 229 GYDIPNLAPNFDILLMSYDFFGAWASLVGFNSPLIATTELPDAWNGW-NVSSARYWQ 287

QY 249 NGATRDVLVGVPPFYGRAWSIEDRSKLGKLGDPAGKMSPPGPGISGEGVLSYIELCOLFOX 308
DB 288 KGMPEKEIIVGMPTYRGWTLNNAISAINPCTSSGPAKITQYVQ-EAGVAYPEFCMLAN 346

QY 309 EEWHIQDYENYAPYNDKIVGYDDIASISCKLAFELKELGVSGVMVNSLENDDFKFGHC 368
DB 347 GATR-YWDSQSQVPLVQGNQWSYDDESFANKMAYVKREGYCGAFVWTLDFDFFNAGC 405

QY 369 GPKN-----PLLNKVNHNMGDEKNSFECIL--GPSTPTPT-----PTTPTTP 410
DB 406 SNSNGQLYPLTISVIAKELGG-----VIIPKGGVTTAPTATTATTATTGTPPMTSAVT 458

QY 411 TTTTPTPTPTPTPTPTPTPT----- 430

reduction on day 3 of pregnancy coincident with transport of the embryo from the oviduct to the uterus, a reproductive stage associated with rising progesterone levels.

-!- SIMILARITY: Belongs to family 18 of glycosyl hydrolases.

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EMBL; U16719; AAC48471.1; --
C3L1_MOUSE
ID C3L1_MOUSE STANDARD; PRT; 381 AA.
AC Q61362;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Chitinase-3 like protein 1 precursor (Cartilage glycoprotein-39)
DE (GP-39) (BRP39 protein).
GN CH3L1 OR BRP39.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euteheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Breast;
RX MEDLINE=95060797; PubMed=7970700;
RA Morrison B.W., Leder P.;
RT "neu and ras initiate murine mammary tumors that share genetic markers generally absent in c-myc and int-2-initiated tumors.";
RL Oncogene 9:3417-3426(1994).
CC -!- FUNCTION: May play an important role in the capacity of cells to respond to and cope with changes in their environment (By similarity).
CC -!- SUBCELLULAR LOCATION: Extracellular (By similarity).
CC -!- SIMILARITY: Belongs to family 18 of glycosyl hydrolases.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

EMBL; X93035; CAA63603.1; --
PIR; S61551; S61551.
DR MGD; MGI:1340899; Ch3l1.
DR InterPro; IPR001223; Glyco_hydro_18.
DR InterPro; IPR001579; Glyco_hydro_18AS.
DR Pfam; PF00704; Glyco_hydro_18; 1.
DR ProDom; PD000471; Glyco_hydro_18; 1.
DR SMART; SM00636; Glyco_18; 1.
DR PROSITE; PS01095; CHITINASE_18; FALSE_NEG.
KW Glycoprotein; Signal.
FT SIGNAL 1 21
FT CHAIN 22 381
FT CARBOHYD 60 60
FT N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 381 AA; 43001 MW; EF6581E8184F0450 CRC64;

Query Match 22.6%; Score 682.5; DB 1; Length 539;
Best Local Similarity 34.4%; Pred. No. 2.2e-30;
Matches 171; Conservative 85; Mismatches 180; Indels 61; Gaps 16;

QY 6 HNDYKPMRIVCVGWTGVSVYHVDPTI--EDIDPEKCTHLMYGFADIKYTIQVFD 63
DB 16 HDGGAH--KLVCFYTNWA-FSRGSAIILPRDLDPFLCHLVFAPASMNQ--IVPKD 70
QY 64 PYQDNHNSWKRGRYFRNLRKLPETLTMISLGGWYEGSEKYSMDAANPTTQQPTQS 123
DB 71 PLD-----EKILYPERKLNKRNGLTKLLSVGGWNGFGRSTKMLSTFSNRERFVK 123
QY 124 VLDFQYKFGDLDDWEYPSGRNLGNPKIDKQNYALVRELKDAFEPHG-----VLLT 176
DB 124 VIALLRTHGFDGLDFFLYPGLR-GSPARDRTWTFVLELLQAFKNEAQLTWPRLLLS 182
QY 177 AAVSGKDKIDRAYDIKELNKLFDWMVMTYDYGWENFYGHNAPLYKRPDDELHTY 236
DB 183 AAVSGDPHVIQKAYDARLLGLLDFISVLSDYLGSGWEKVTGNSPLFSPLGDPK----- 237
QY 237 ENVNTMTHYLLNGATRLKLVGVPFYGRAMSIEDRSKILGDPAGKMSPPGFTSGEGV 296
DB 238 -SSAVASYWQLGVPPKELINGLTYGRTTHLLRASQNELGAGAPASPGYTKQAGF 296
QY 297 LSYIELCOLFQKEHHIYDEYFNAPYGYNDKIWGYDDLASISCKLAFLKELGVSGVMV 356
DB 297 LAYEVCVSFQAKRWINDQY--VPYAFKGEWGYDDAISFGYKAPFIKREHFGAMV 354
QY 357 WSLNDNDPKGH-CGP-KNPLLNKVNMMINGDEKSPFICILGFTTTPP-----TTTTPP 410
DB 355 WTLDLDDFGNPGCGTGPFLAHTLNNLVNDEFSS-----TPSPKFWFSTAVNNS 404
QY 411 TTTTPPSTPTTTPPTTP-----TTTPSTPTTTPPTTPPTTP-----T 455
DB 405 RTGPEMPTTRDLTGLGILPGGEAVATETHRKSAATTTTPRGETAFTPTPLSSGRT 464
QY 456 PAPPTSTPSPTTHTS 472
DB 465 AAPEGKTESPGKPLTS 481

RESULT 9
C3L1_MOUSE
ID C3L1_MOUSE STANDARD; PRT; 381 AA.
AC Q61362;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Chitinase-3 like protein 1 precursor (Cartilage glycoprotein-39)
DE (GP-39) (BRP39 protein).
GN CH3L1 OR BRP39.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euteheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Breast;
RX MEDLINE=95060797; PubMed=7970700;
RA Morrison B.W., Leder P.;
RT "neu and ras initiate murine mammary tumors that share genetic markers generally absent in c-myc and int-2-initiated tumors.";
RL Oncogene 9:3417-3426(1994).
CC -!- FUNCTION: May play an important role in the capacity of cells to respond to and cope with changes in their environment (By similarity).
CC -!- SUBCELLULAR LOCATION: Extracellular (By similarity).
CC -!- SIMILARITY: Belongs to family 18 of glycosyl hydrolases.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

EMBL; X93035; CAA63603.1; --
PIR; S61551; S61551.
DR MGD; MGI:1340899; Ch3l1.
DR InterPro; IPR001223; Glyco_hydro_18.
DR InterPro; IPR001579; Glyco_hydro_18AS.
DR Pfam; PF00704; Glyco_hydro_18; 1.
DR ProDom; PD000471; Glyco_hydro_18; 1.
DR SMART; SM00636; Glyco_18; 1.
DR PROSITE; PS01095; CHITINASE_18; FALSE_NEG.
KW Glycoprotein; Signal.
FT SIGNAL 1 21
FT CHAIN 22 381
FT CARBOHYD 60 60
FT N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 381 AA; 43001 MW; EF6581E8184F0450 CRC64;

Query Match 22.6%; Score 680; DB 1; Length 381;
Best Local Similarity 37.1%; Pred. No. 2e-30;
Matches 141; Conservative 75; Mismatches 130; Indels 34; Gaps 10;

QY 15 RIVCYGVGTSVYHK-VDPYTIEDIDPFKCTHLMYGFADIKYTIQVDPDQDNHNSW 73
DB 23 KLVCFYTSQYREGVSGSFLDPAIQFLCTHIIYSPANIS-----SDNMLSTW 70
QY 74 E---KRGYFRFNLRKLPETLTMISLGGWYEGSEKYSMDAANPTTQQPTQSVDLQOE 130
DB 71 EWNDESNYDKLNKTRNTNLKLLSVGGWKFGEKFSFIASNTERTAFVRSVAPFLRS 130
QY 131 YKFDGLDDWEYPSGRNLGNPKIDKQNYALVRELKDAF---EP--HGVLTTAAVSPGKD 184
DB 131 YGFDGLDLAWLYPRLR-----DKQFESTLKLNELNAEFTKEVQGREKLLLSAALGAKV 184
QY 185 KIDRAYDIKELNKLFDWMVMTYDYGWENFYGHNAPLYKRPDDELHTYFNVTM 244
DB 185 AIDTGYDIAQIAQLDIFNLMTYDFHGWRFQITGHSPFQGGKDT-RPDYNSVNVAVQ 243

SEQUENCE OF 22-39.

MDLINE=94058981; PubMed=8240241;

Malette B., Bieau G.;

"Biochemical characterization of hamster oviductin as a sulphated zona pellucida-binding glycoprotein.";

Biochem. J. 295:437-445(1993).

-1- FUNCTION: Binds to oocyte zona pellucida in vivo. May play a role in the fertilization process and/or early embryonic development. Might act as a protective secretion influencing the first steps of the reproductive process necessary for the normal triggering of fertilization and early embryonic development.

-1- SUBCELLULAR LOCATION: Secretory granules.

-1- TISSUE SPECIFICITY: Oviduct.

-1- PM: HIGHLY O-GLYCOSYLATED AND ALSO N-GLYCOSYLATED.

-1- SIMILARITY: Belongs to family 18 of glycosyl hydrolases.

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EMBL; D32218; BAA06977.1; --

EMBL; U15048; AAC3584.1; --

InterPro; IPR001223; Glyco_hydro_18.

InterPro; IPR001579; Glyco_hydro_18AS.

Pfam; PF00704; Glyco_hydro_18; 1.

ProDom; PD000471; Glyco_hydro_18; 1.

SMART; SM00636; Glyco_18; 1.

PROSITE; PS01095; CHITINASE_18; FALSE NEG.

Glycoprotein; Fertilization; Repeat; Signal.

SIGNAL 1 21

FT CHAIN	22	671	OVIDUCT-SPECIFIC GLYCOPROTEIN.
FT DOMAIN	490	609	8 X 15 AA TANDEM REPEATS.
FT REPEAT	490	504	1.
FT REPEAT	505	519	2.
FT REPEAT	520	534	3.
FT REPEAT	535	549	4.
FT REPEAT	550	564	5.
FT REPEAT	565	579	6.
FT REPEAT	580	594	7.
FT REPEAT	595	609	8.
FT CARBOHYD	402	402	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD	511	511	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD	536	526	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD	541	541	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD	556	556	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD	571	571	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD	586	586	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT	26	26	C -> A (IN REF. 4).
FT CONFLICT	33	33	H -> I (IN REF. 4).
FT CONFLICT	137	137	D -> G (IN REF. 2 AND 3).
FT CONFLICT	153	153	R -> Q (IN REF. 2 AND 3).
FT CONFLICT	165	165	F -> Y (IN REF. 2 AND 3).
FT CONFLICT	193	193	Q -> L (IN REF. 2 AND 3).
FT CONFLICT	531	545	MISSING (IN REF. 2 AND 3).
FT CONFLICT	595	595	T -> I (IN REF. 2 AND 3).
FT CONFLICT	671	73250	MM; BB57E0E514EC1972 CRC64;
FT CONFLICT	671	73250	MM; BB57E0E514EC1972 CRC64;

SEQUENCE 671 AA; 73250 MW; BB57E0E514EC1972 CRC64;

Query Match 22.5%; Score 677.5; DB 1; Length 671;

Best Local Similarity 34.1%; Pred. No. 5.1e-30;

Matches 175; Conservative 80; Mismatches 187; Indels 71; Gaps 15

QY 15 RIVCYGTVSWYHKVDPIYI--EDIDPEKCTHLMYGFAKIDYKYVIOVDFPVQDDNHS 72

DB 23 KLYCYPTNWA-HSRPVPASLPRDLDFLCTHLIFAFASNNQI----VANNLQD----- 73

QY 73 WEKRGYERFNNLKNPELTTMISLGGYEGSEKYSQDMAANFYRQOFIQSVLDFLQYK 132

74 FYITVDFENKVFEPNATKTLISVGGNNGTSPRTTMTLSTLASRPFKIGSVVSFLRTG 132

QY	177	AAVSPGKOKIDRAYDIKEINKLFDMNWNVTYDYGWENFYGHVAPLYKRPDSTDELHTY	233
DB	183	AAVSGVPHIVQTSYDVRFLGRLLDITNVLSDYHLGWSWERTGHNSPLFSLEPDPK	237
QY	237	FNVNVTTHVYLNAGATRDKLGVNGVPFYCGRAWISIEDRSKLLGDPAKMSPPGFISSGEGV	296
DB	238	-SSAVAMNWRKLGAPSEKLIINGITGYQRTFRLKASKNGLOARAIQAPSPGYKTKQEGF	296
QY	297	LSYIELCQLF--QKEBWHIQYDEYVNAFYNDKIWVGYYDDLASISCKLAPLXELGVSGV	354
DB	297	LAYFELCSFWGAKKH---IDYQVVPYANKGEWGYDNAISFYKAWFIRREHFGGA	352
QY	355	MWVSLNDPKG-HCGP-KNPLLNKVHNMINGDEKNSFECILGPSTTPT--PTTPTTP	410
DB	353	MWVTLDMDDVRGTFCTGCTGFPFLVYVLLNDILVRAEFS-----STSLPQFWLSSAVNSS	404
QY	411	TTTTPT	455
DB	405	STDPERLAVTTAATWTDKSLIPGSGAGVTEIHGKCNENITIPRGTVTPTKETVSLGKHT	464
QY	456	----PAPTSPPTTTEHTSETP--KYTTVVVDGH	484
DB	465	VALGEKTEITGAMTWSVGHQSWPTCEKALTPV-GH	499
DB		STANDARD; PRT; 383 AA.	
RESULT 14			
C3L1 HUMAN			
ID_C3L1 HUMAN			
AC	P36222; P30923;		
DT	01-JUL-1993 (Rel. 26, Created)		
DT	01-JUN-1994 (Rel. 29, Last sequence update)		
DT	10-OCT-2003 (Rel. 42, Last annotation update)		
DE	Chitinase-3 like protein 1 precursor (Cartilage glycoprotein-39) (GP-		
DE	39) (39 kDa synovial protein) (VKL-40).		
GN	CHI3L1.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.		
RC	TISSUE=Cartilage;		
RC	MEDLINE=97386591; PubMed=8245017;		
RX	MEDLINE=94064659; PubMed=8245017;		
RA	Hakala B.E., White C., Recklies A.D.;		
RA	"Human cartilage gp-39, a major secretory product of articular		
RT	chondrocytes and synovial cells, is a mammalian member of a chitinase		
RT	protein family.";		
RL	J. Biol.,Chem. 268:25803-25810(1993).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Blood;		
RC	MEDLINE=97386591; PubMed=9244440;		
RX	MEDLINE=97386591; PubMed=9244440;		
RA	Renli W., Krause S.W., Andressen R.;		
RT	"Molecular characterization of the gene for human cartilage gp-39		
RT	(CHI3L1), a member of the chitinase protein family and marker for		
RT	late stages of macrophage differentiation.";		
RL	Genomics 43:221-225(1997).		
RN	[3]		
RP	SEQUENCE OF 22-45.		
RC	MEDLINE=90328983; PubMed=2375755;		
RX	MEDLINE=90328983; PubMed=2375755;		
RA	Nyirkos P., Golds E.E.;		
RT	"Human synovial cells secrete a 39 kDa protein similar to a bovine		
RT	mammary protein expressed during the non-lactating period.";		
RL	Biochem. J. 269:265-268(1990).		
CC	!- FUNCTION: May play an important role in the capacity of cells to		
CC	respond to and cope with changes in their environment.		
CC	!- SUBCELLULAR LOCATION: Extracellular.		
CC	!- TISSUE SPECIFICITY: Present in articular chondrocytes, synovial		
CC	cells as well as in liver. Undetectable in muscle tissues, lung,		
CC	pancreas, mononuclear cells, or fibroblasts.		
CC	!- PM: Glycosylated.		
CC	!- SIMILARITY: Belongs to family 18 of glycosyl hydrolases.		
CC	-----		


```

Db      183 AAVSGVPHIVQISYDVRFGRLLDFINVLSYDLHGSWEKFTGHSFLSLPEDPK----- 237
Qy      237 FNVNYTMHYLLNNGATRDKLNVGVPPFYGRAWSIEDRSKLKLGDPKAGMSPPGFISGEEGV 296
Db      238 -SSAYAMNYWRKLGAPSEKLIWGIPTYGRTFLLKASKNGLQATAIGPASPGKYTKQAGF 296
Qy      297 LSYIELCQLF--QKEEWHIOYDEYNAPGYNDKIWVGYYDDLASISCKLAFLKELGVSGV 354
Db      297 LAYFEICSPVMGAKKHW----IDYQVVPYANKGEWVGYYDDAISPSYKAWFIRRBHFGGA 352
Qy      355 MWWSLENDDFKG-HCGP-KNPLLNKVHNMINGDEKNS-----PECILGPSTTTP---- 401
Db      353 MWYTLDDMDVRGTFCGTGPFPLVYVMNDILVRAEFSSTSLPQFWLSSAYNSSSTDPERLA 412
Qy      402 -----TPTTTPPTPT----- 411
Db      413 VTKAWTTDIKILPPGGEAGVTEIHGKCENMTTTPRTIVTPTKETVSLGKHTVALGEKTE 472
Qy      412 ----TPTTTPSPPTPTTTPSPPTTPTTPS--PTTPTTTP-----SPTTPTPT-----TP 454
Db      473 ITGATTWTSVGHQSMTPEKALTPVGHQSLELPGKKTLTPVGHQSVTTGQKTLISVGYHSV 532
Qy      455 TPAPTST----PSPTTTEHTSETPKYTTYVDGH 484
Db      533 TPGEKTLTPVGHESVTPVSHQSVSPGGMTMPVH 566

Search completed: March 22, 2004, 06:53:06
Job time : 21.5581 secs

```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 22, 2004, 06:40:28 ; Search time 34.8594 Seconds
(without alignments)
1479.047 Million cell updates/sec

Title: US-09-662-293-21

Perfect score: 3014

Sequence: 1 SIKRDNDYSKNPMRIVCV.....IMPCPGTIWQCKLTIGE 536

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 78.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1007	33.4	525	T44445	chitinase (EC 3.2.2)
2	869	28.8	1635	T14075	chitinase (EC 3.2.2)
3	834	27.7	554	A56596	chitinase (EC 3.2.2)
4	801.5	26.6	483	A53918	chitinase (EC 3.2.2)
5	705.5	23.4	617	T15408	hypothetical prote
6	692.5	22.6	539	T46470	estrogen dependent
7	673	22.3	537	S57197	oviduct-specific g
8	687.5	22.1	654	T38605	oviductal glycopro
9	660	21.9	383	A49582	cartilage glycopro
10	650	21.6	383	S51327	heparin-binding gl
11	646.5	21.4	405	S61551	breast-regressing
12	608	20.2	399	S27879	secretory protein
13	604.5	20.1	504	A38221	chitinase (EC 3.2.2)
14	588	19.5	599	D32784	chitinase BH0916 [
15	561	18.6	699	A38368	chitinase (EC 3.2.2)
16	560	18.6	1215	T43916	chitinase A [impor
17	456.5	15.1	831	T00323	chitinase (EC 3.2.2)
18	432.5	14.3	1484	T29275	hypothetical prote
19	428	14.2	869	T44440	chitinase (EC 3.2.2)
20	427.5	14.2	849	D82510	chitinase VCA0027
21	424.5	14.1	2025	T03884	hypothetical prote
22	414.5	13.8	563	S60651	chitinase precursor
23	411	13.6	423	J01975	chitinase (EC 3.2.2)
24	408.5	13.6	561	A25090	chitinase I precur
25	405.5	13.5	424	S68121	chitinase (impor
26	405	13.4	546	F94238	chitinase - fungus
27	402.5	13.4	423	S51369	chitinase B homolo
28	402.5	13.4	756	AB1452	chitinase B homolo
29	399	13.2	756	AB1088	chitinase B homolo

30 393 13.0 633 2 T24898 hypothetical prote
31 391.5 13.0 558 2 T30418 chitinase (EC 3.2.2)
32 388 12.9 424 2 S47133 chitinase (EC 3.2.2)
33 388 12.9 820 2 A40633 chitinase (EC 3.2.2)
34 385 12.8 799 2 PC4106 chitinase (EC 3.2.2)
35 381.5 12.7 452 2 JC4038 47K Glycoprotein p
36 380 12.6 755 2 T20950 hypothetical prote
37 378 12.5 765 2 T35719 chitinase - Strept
38 377.5 12.5 550 2 T10393 chitinase (EC 3.2.2)
39 371.5 12.3 398 2 T04761 chitinase homolog
40 368.5 12.2 1088 2 D82246 probable chitinase
41 367.5 12.2 511 2 S61166 probable membrane
42 365 12.1 379 2 T04762 chitinase homolog
43 364.5 12.1 552 2 T41863 chitinase chi-A or
44 360.5 12.0 551 2 G72865 chitinase - Autogr
45 356.5 11.8 427 2 JC4565 chitinase (EC 3.2.2)

ALIGNMENTS

RESULT 1

T44445
chitinase (EC 3.2.1.14) [imported] - African malaria mosquito
C:Species: Anopheles gambiae (African malaria mosquito)
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jan-2000
C:Accession: T44445
R:Shen, Z.; Jacobs-Lorena, M.
submitted to the EMBL Data Library, June 1997
A:Reference number: Z22771
A:Accession: T44445
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-525 <SHE>
A:Cross-references: EMBL:AF008575; PIDN:AAB87764.1
A:Experimental source: adult; gut
C:Genetics:
A:Gene: chi-1
C:Keywords: glycosidase; hydrolase

Query Match 33.4%; Score 1007; DB 2; Length 525;
Best Local Similarity 39.5%; Pred. No. 2.9e-55;
Matches 210; Conservative 86; Mismatches 178; Indels 59; Gaps 12;

QY 6 HNDYKSNPMRIYCYVGTWSVHKVD-PYTIEDIDPFKTHLMYGFADKDEYKYYTQVDFP 64
Db 23 HKAASAEGKKVCYVGTWAVYRPGNGRYDIEHIDPSLCTHLMYGFEGINE-DATVRIIDP 81
QY 65 YQDDNHSWEKGYERFNNLRKNBELTMSLGGWYEGSEKYSQMAANPTVYRQOQISQV 124
Db 82 YLDLEEN-WGRGHIKRFVGLKNVPGFKTLAAIGGNWEGSRKFSMAASGEURKRFISDC 140
QY 125 LDPLQYKFDGLDWEYFGSLGNPKIDKQNYLALVRELKDAFPHGYLLTAASVPGKD 184
Db 141 VAPCQRHGFGLDLDWEYFPAQDGNPLIDRDHQAQLVEEMREEFHYGLLLTAASVDF 200
QY 185 KIDRAYDIKELAKLFDMNNVMTYDYGWENFYGHNAPLYKRPDETDELHTYFNNVYTMH 244
Db 201 SAGVSVDIIRKSHFHLNVMYDMGAWDSYCGINAPLYRGSADTDLRLGQINVNASTH 260
QY 245 YLNNAGATDKLVMGVFPYFGRAWSTEDRSKLKGPDAKMGSPPGFISGEGVLSTELCQ 304
Db 261 FWLAQOCTGRKLVGLPIYGRNFTLASAANTQIGAPTVGCGTVGYRTREPGVNGYNEFCE 320
QY 305 LFQKEWHIQYBYYNAPYGYNDKIVWGYDDIASCKLAFKLKELGVSGVMWVSLNDDF 364
Db 321 KLATEAWDLRWSEEQVQPYAVRNQWGYDDLSVQLKVLDDQLGGAMVWSLTDFF 380
QY 365 KGHC-GPKPPLLKNVHNMINGEKNSFECILGSPSTTTPTTPTTPTTPTTPTTPTTPTT 423
Db 381 LGVCGGRYFELMHEIKSLVNGGT-----PSITMFPFSVAPIT-----STVAGTTT 426
QY 424 TTPSPPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTT 483

Db 427 TTGTGANGTQPTT--SDAPNHTTTTTEGNGPTRPPSG-----DG 468
 Qy 484 HLIKCY--KEGDIPHPNIIHKYLCV-----EFVNGGWVHIMPCCPGTIW 526
 Db 469 ---PCAGRGYGFPHPTNCARYICLTADTYEFT-----CPTGTLF 507

RESULT 2
 T14075
 chitinase (EC 3.2.1.14) - yellow fever mosquito
 C:Species: Aedes aegypti (yellow fever mosquito)
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
 C:Accession: T14075
 R:de la Vega, H.; Specht, C.A.; Liu, Y.; Robbins, P.W.
 Insect Mol. Biol. 7, 233-239, 1997
 A:Title: Chitinases are a multi-gene family in Aedes, Anopheles, and Drosophila.
 A:Reference number: Z17872
 A:Accession: T14075
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1635
 A:Cross-references: EMBL:AF026492; NID:G2564720; PID:G2564721; PIDN:AAB81850.1
 C:Genetics:
 A:Gene: CHT2
 A:Introns: 462/3; 524/3; 618/1; 951/3; 1151/2
 C:Keywords: glycosidase; hydrolase; polyaccharide degradation

Query Match 20.8%; Score 869; DB 2; Length 1635;
 Best Local Similarity 34.3%; Pred. No. 5e-46;
 Matches 196; Conservative 95; Mismatches 196; Indels 84; Gaps 18;

Qy 2 IKRDHNDYKNPM-----RIVCVGWSVYHKVD-PYTIEDIDPKCTHLMVGPAKIDE 54
 Db 650 INKTSQNDNAIESVDYKVCCFTNWAIRQNGKYLPEIDADLCHIVVGFVAVLR 709
 Qy 55 YKVTIOVEDPYQDDNHSW---EKRGYERFNNLEKNPELTMTISLGWYEGS-EKYSDM 110
 Db 710 DLRLVK-----PHDSWADIDNRFYRVVYKKGKVT--VAIGWNDSAGDKYSL 759
 Qy 111 AANPTYQOFTQSULDFLQYKFGDLDMWYPGSRLGNPK----IDKQNYLALVRELKD 166
 Db 760 VRSAAARQKFTADVAFTEKYFGDLDMWYPCWQVCKGFSDEKGFASLVVELSQ 819
 Qy 167 AFEPHGVLITAAVSPGKDKIDRAVDIKELNKLFDMMNMTYDVHGGWENFYGHNAPLYKX 226
 Db 820 AFKPKGLLLSAVSPSKVDEGVYVLTSDYMDWIAVMAYDHQGDWKKTGHVAFMYEH 879
 Qy 227 PDETDELHTYENVAVTWHYILNNGATDKLVGVYFPFGRAWSIDRSKLGDPKXGMP 286
 Db 880 PDDFEXT---FNANFTIHWLEKADPKLVGMGPMYQGSFSLADNKEHGLNAKTYGGGE 936
 Qy 287 PGFTSGEGLVSYIELCOLFOKEBWHIOYDEYN-APYGNDKILWGYDDLIASISCKLAF 345
 Db 937 AGESTRARGFLSYVEICANIRKKWTAVARDKGRMGFYAYKGQWVSFDDQYIMIRHKSEY 996
 Qy 346 LKELGVSGVWVWSLENDPKHCG-PKNPLNKKVHNNINGDEKNSFCIL--GPSITPTT 402
 Db 997 VKAMGLGGMWALDLDLDFNLDCESYPLLRTINRVLNRYVPGPGPCVLEKSPQREBR 1056
 Qy 403 PTTTPTTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTT 462
 Db 1057 PTRPPTS-----TTPETTRPSTTSRATTTTIT--TTTRPTTTTTRATSAR 1104
 Qy 463 PSPTTTHTSETPKY-----TTYVDGHLIKCYKEGDIPIHPTNTHKYLVCFVNGGW 513
 Db 1105 PIVTTT---NVPSQEIANEVDEPTCTDGRLF-----VPHPTDCKNYVICQYCKG-- 1150
 Qy 514 WWHIMCPSPGIW-----CQKLT 532
 Db 1151 -----LCRPGGLVSWVDHCDWQSQNCRNKQT 1176

A:Reference number: A53918; MUID:94342256; PMID:8063715
A:Accession: A53918
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-483 <XRI>
A:Cross-references: GB:U10422; NID:G533504; PIDN:AAA61639.1; PID:G533505
C:Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 26.6%; Score 801.5; DB 2; Length 483;
Best Local Similarity 38.0%; Pred. No. 1.6e-42;
Matches 158; Conservative 82; Mismatches 157; Indels 19; Gaps 8;

QY	12	NPWRIVCVGTWSYHKVD-PYTTIEDIDPFKCTHLMYGFAXIDYKKTIOVFDPQDDNH	70
Db	20	SPNKWCYFGAASYROGNGKFDINGIDPTLCTHLIYSFVGVN--GKDVLDPSWDLPG	77
QY	71	NSWEKRGVERPNNLRKNPELTLMISLCGWEGSEKYSDMAANPTYROCFQTSQSLDFLQE	130
Db	78	N---LDGFGKETSRLKKNPSVKLIWVAVGGWAGSVFPFSOMASDOATREAFQNVVKELQQ	134
QY	131	YKFDGLDLDWEYPGSRIGNPKXIDKQNVIALVRELKDAPEPHFGYLLTAAVSPGKDIDRAY	190
Db	135	YQFDGFDIDWEYPAQRGSSP-ADVKNMVKLCKALKGAPVQHDYILSAAVAAPETSAKSY	193
QY	191	DIKELNKLFDWNNVMTYDHYHGGWENFYG-HNAPHYKRPDEDELDLHTFNNVYTHYYLNN	249
Db	194	DIAEWSQYLDFTNLMTYDFHGFWDGHTGMHAPSPASSSHSDSGNELK--LNVKAAVKYMLQN	251
QY	250	GATRDKLVMGVPFFYGRAWSIEDRSKLLGDPKAGMSPPGFTSGREGVLSTELCOLFOKE	309
Db	252	GVPKEKLVGVGPAYGKSFLLSNPKNLGUGAPVSGAGTAGPYTGNGLLGYNEICEMQKAG	311
QY	310	EWHTQYDYBYNAPGYNDKIVWGYDDDLASISCKLAFKLKELGVSQVWVMSLENDDFPKHCG	369
Db	312	DWEVVQDNEKGVPFAVKNQVNSFDDLAAIKAKAQFIKQEGGLGGAAVWSIETDDDFKGLCG	371
QY	370	PKNELLNKNVNNINGDEKNSFECILGPSTT---TPPTPTPTPTPTPTPTPTPTPTPT	422
Db	372	EKYFVFLKALNSVLGRGGSSS-----PAETKRNKNVDPDQAPRFSFAEDSAPAE	421

RESULT 5

```
Tt15408
hypothetical protein C04F6.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: Tt15408
R:Nhan, M.
submitted to the EMBL Data Library, December 1995
A:Description: The sequence of C. elegans cosmid C04F6.
A:Reference number: Z18346
A:Accession: Tt15408
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-617 <NHA>
A:Cross-references: EMBL:U42835; NID:g1125760; PID:g1125762; PIDN:AAA83586.1; CESP:C04F6.3
C:Genetics:
A:Gene: CESP:C04F6.3
A:Introns: 28/1; 66/2; 504/1

Query Match      23.4%   Score 705.5; DB 2; Length 617;
Best Local Similarity 30.2%; Pred. No. 2.le-36;
Matches 178; Conservative 90; Mismatches 210; Indels 111; Gaps 19;

Qy    18 CYGTWNSVIHK-VDPYTIEDIDPPKCTHLMYGPAKIDEYKYTTIQVDFPYQDDNHNSWEKR 76
      ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Db    57 CYFTNWAQYRGRAKFVPEDYTPGLCTHLIFAFGMNA-DYTVRAYDP--ADLENDWAGE 113
      ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||

Qy    77 G-YERFNRLKNPELTMTISLGWYSGSEKYSDMAANPTVRQFIQSVLDFLQEYKFDG 135
      ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Db    114 GWYRVNKLKTDTQLTKLSFGWSFGTALFQGMASASRRKFVIDSATFTVRTWGFDG 173
      ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||

Qy    136 LLDLWEYFGSLGNPKIDQNLYALVRELKDIAFEFHG-----YLTAAVSPGKKIDR 198
```

RESULT 6

I46470
estrogen dependent oviduct protein precursor - sheep
C/Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C/Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 05-Nov-1999
C/Accession: I46470
R:DeSouza, M.M.; Murray, M.K.
Endocrinology 136, 2485-2496, 1995
A/Title: An estrogen-dependent secretory protein, which shares identity with
and embryo development.
A/Reference number: I46470; PMID:7750470
A/Accession: I46470
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-539 <DS>
A/Crossa-references: EMBL:U16719; NID:5885600; PIDN:AAQC48471.1; PID:g895601

Query Match	22.6%;	Score 682.5;	DB 2;	Length 539;
Best Local Similarity	34.4%;	Pred. No. 4.7e-35;		
Matches	171;	Conservative 85;	Mismatches 180;	Indels 61; Gaps 16;
Qy	6	HNDSKNPMRIVCVGTWSTVYHKVDPTI--EDIDPEKCTHLMYGFPAKIDEXKYTIQVFD	63	
Db	16	HHDGAAH--KLVCYFTTWA--FSRPGSASILPRDLDPFLCTHLVFAPASMNNO--IVPKD	70	
Qy	64	PYQDDNHSWEKRGYEFNNLRKNPELTWISLGWVYEGSEKYSIDMAANPTYRQOPIQS	123	
Db	71	PLD-----EKILYPEFKLRNKGKTKILLSVGGWNFGSRTKMLSTFSNRERFVKS	123	
Qy	124	VLDFLOQYKDGDLDDWEYPSRSLGNPKIDKQNTALALVRELKDAFEPHG-----YLLT	176	
Db	124	VIALLRTHGPDGLDLFLYPLGLR--GSPARDENWTFVLLLELLQAFKNEAQLTMERULLS	182	
Qy	177	AAVSPFGKDKIDRAYDIKELNKLFDMMNMWTVDYHGGWENFVGHNAPIYKRPEDETLHTY	236	
Db	183	AAVSGDEPHVIQAYDARLLGRLLDFISVLSDYLGHSWEKVTGHNSTPLSLPGDPK-----	237	
Qy	237	FNNVYTHYYLNGATDKLWGVVPFYCGRAWISIDRSKLGLGDPAKMGSPPGFISGEEGV	296	
Db	238	--SAYAMSYNFOILGVVPEKLMGLPTVGRTHLLRASONEILCAGAAGPASPCKTTKOAGF	296	

QY 245 YYLNNGATRDKLVMGVFFYGRAWSIEDRSKLLGDPKAGMSPPGFISGEGVLSYIELCQ 304
DB 244 YNTRLGAQASKLLMGITPGTKGFTLAS-SENQIGAPISGEGLPGRFTKEAGTLAGYVEICD 302
QY 305 LFKSEWHIOYDEYNAPGYNDKIVGWDDLASISCKLAFELKELGVSGV-----MWSLE 360
DB 303 FLKGAEVHRLSNE--KVPFATKGNOWGYEDKESVKNYGFLEKELKAGAMCGHWIWI- 359
QY 361 NDDPKGCHCPKPNLLKNVHNGDEKNSFCILGSPSTTTPPTTP 407
DB 360 ----SGHCQPKN-----SSRPTPSRMP 378

RESULT 12

S27879
Secretory protein YM-1 precursor - mouse
C:Species: Mus musculus (house mouse)
C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 22-Jun-1999
C:Accession: S27879
R;Chang, N.C.A.; Liu, C.H.; Chang, A.C.
Submitted to the EMBL Data Library, June 1992
A:Description: Molecular characterization of a secretory protein (YM-1) transiently expressed in *Brugia malayi*
A:Reference number: S27879
A:Accession: S27879
A:Molecule type: mRNA
A:Residues: 1-399 <CHA>
A:Cross-references: EMBL:M4584; NID:g202441; PIDN:AB62394.1; PID:g202442
C:Superfamily: Streptomyces chitinase chi40
F;1-21/Domain: Signal sequence #status predicted <SIG>
F;22-399/Product: secretory protein YM-1 #status predicted <MAT>

Query Match 20.2%; Score 608; DB 2; Length 399;
Best Local Similarity 36.3%; Pred. No. 1.4e-30;
Matches 141; Conservative 67; Mismatches 140; Indels 40; Gaps 14;

QY 15 RIVCVGVTSVYHKVD-PYTIEDIDPFCKTHLMYGAFT--DEYKTYIQVDPYQDDNHN 71
DB 23 QLMCYTWSAKORPIEGSPFGNIDPCLCHLIYAFAGQNEITYT-----H 70
QY 72 SWEKRGYERFNNLR-LKNPELTMI SLGWYEGSEKYSIDNANPTYRQOFIQSVLDFLOE 130
DB 71 EQDLRDEALNGLKDKQNTLKTLLAIGWKFGPAPFSAVMSVTPQNRQIFQSVIRFLAQ 130
QY 131 YKFDGLDWEYPSRIGNPKIDKQNYLALVRELKDAPEPHG-----YLLTAASVPGK 183
DB 131 YNFDGLNLDQYQGRS-GSPDKDHLFSLVKEMKAFEESEVEKDIPRLTLT---STGA 186
QY 184 DKIDRAYD-IKELN--KLFPDMVMVYDHYHGGWENFVGHNAPLYKSPDETDLHTYFNVN 240
DB 187 GIIDVIKSGTRSLNCLSLDYIQMTYDLHDPKDGTYGNSPLYKSPYDYGK-SADLNVD 245
QY 241 YTHYLLNNGATRDKLVMGVFFYGRAWSIEDRSKLLGDPKAGMSPPGFISGEGVLSYI 300
DB 246 SIISYWKDNGAASEKLVGPAVGHFTILSDPKTGIGARTISTGPPGKYTDSGLLAY 305
QY 301 ELCOLFQK---EEWHIOYDEYNAPGYNDKIVGWDDLASISCKLAFELKELGVSGV 357
DB 306 EVCTFLNEGATEVW---DAPQEVYAYQGNWGYDNVRSFKLKAQWLKDNLLGAVVW 361
QY 358 SLENDDFKG-HCGPKN-PLLNKVNMIN 383
DB 362 PLDMDFSGSFCHQHFPLTSLTKGLN 389

RESULT 13

A38221
Chitinase (EC 3.2.1.14) MF1 - nematode (*Brugia malayi*)
C:Species: *Brugia malayi*
C>Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
C:Accession: A38221
R;Fuhrman, J.A.; Lane, W.S.; Smith, R.F.; Piessens, W.F.; Perler, F.B.
Proc. Natl. Acad. Sci. U.S.A. 89, 1548-1552, 1992
A:Title: Transmission-blocking antibodies recognize microfilarial chitinase in *brugian*

A:Reference number: A38221; MUID:92179220; PMID:1542646
A:Accession: A38221
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid; protein
A:Residues: 1-504 <PUH>
A:Cross-references: NID:g156063; PIDN:AAA27854.1; PID:g156064
A:Note: sequence extracted from NCBI backbone (NCBIP:85345)
C:Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 20.1%; Score 604.5; DB 2; Length 504;
Best Local Similarity 30.1%; Pred. No. 3.1e-30;
Matches 156; Conservative 86; Mismatches 208; Indels 69; Gaps 17;

QY 18 CYVGTWSVYHKVD-PYTIEDIDPFCKTHLMYGAFTDEYKTYIQVDPYQ-DNHNHSEW 75
DB 27 CYTWNAAQYRDGEGKPLGNIPNGLCTHILYAFKVD-----LGDSKPFEDNDETEWSK 82
QY 76 RGYERFNNLRKQPELTMI SLGWYEGSEKYSIDNANPTYRQOFIQSVLDFLOEYKFDG 135
DB 83 GMSAVTKLRETNPGLKVLISYGGYNFGSAIFGTIAKSAOKTERFIKSAFAKKNFNG 142
QY 136 LLDLWEYP-GSRLGNPKIDKQNYLALVRELKDAPEPHGYLLTAASVPGKDKIDRAYDIKE 194
DB 143 FDLWEIPVGVAEHAKLVEAMKTAFFEAKTSGKQR-LLLTAASVAGKTIDGSYNVES 201
QY 195 LNKLFDMVMVYDHYHGGWENFVGHNAPLYKRPDETDLHTYFNVNVTMYYLNNGATRD 254
DB 202 LGKNFDLLFLMSYDLHGSWEKVDLHGLKHTPKGEVSGI-GIFNTEPAADYWASKGMPKE 260
QY 255 KLVNVPYFYGRAMSIEDRSKLLGDPKAGMSPPGFISGEGVLSYIELCQFQKEEWHIQ 314
DB 261 KIITGIPWYAQWTLDPNSETAIGAAASRPSSASKTNPAGTASWEICKYKEGGKETV 320
QY 315 YDEYNAPGYNDKIVGWDDLASISCKLAFELKELGVSGVVMWSLENDDFKG-HCGP-KN 372
DB 321 HQEGVGA-YVMYKGDWYDNEETIRIMKWLKRGYGGAFIMALDDDFDTGKSCGKGPY 379
QY 373 PLLNKHVMINGDEKNSFCILGSPSTTTPPTTPTTPTTPTTPTTPTTPTTPTTPTTPT 432
DB 380 PLLNNAISSELGESN-----PEITTEPSITETAYETDEEE----- 418
QY 433 TTPSPPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPT 488
DB 419 -----TSEAYDTD-----ETESET-EATTYDITDETEGQ-EC 451
QY 489 -YKEDIHPNINHYLVCEFNWGWVHIMPCPPGTIW 526
DB 452 PERDGLPPTDCHLFIOQ-----ANNIAYVMQCPATTFF 486

RESULT 14

D83764
Chitinase BH0916 [imported] - *Bacillus halodurans* (strain C-125)
C:Species: *Bacillus halodurans*
C>Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C:Accession: D83764
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Fujii, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and
A:Reference number: A83650; MUID:20512582; PMID:11058132
A:Accession: D83764
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-599 <STO>
A:Cross-references: GB:AP001510; GB:BA000004; NID:g10173440; PIDN:BA04635.1; GSPDB:GN001
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH0916

Query Match 19.5%; Score 588; DB 2; Length 599;
Best Local Similarity 29.6%; Pred. No. 4.1e-29;
Matches 179; Conservative 91; Mismatches 200; Indels 134; Gaps 29;

QY	10	SKNPMRIVCYVGTWSVYHKVDYPTIBDIPFKCTHLMYGFAPK-----51
Db	36	SDDOYKIVAVYPSWGAAGR--DYQWVIDASAKISHINYAFANTCWDGRHGNPDPAQNPQ93
QY	52	-----IDEXYKTIQVDPDYOD-----DNNHSEK--RG-YERFNNLRKLNPELITM94
Db	94	TWSQCODENGVIDVPNGSILVMGDPMIDAKQNGPDGDEPLRGNPKQLNKLEBPHLXTL153
QY	95	ISLGGWEGSEKYSMAANPTYROOFQSVLDFLQCYKFGDGLDWEYP--GSRIGNPK-151
Db	154	ISVGGW-TWSNRFSDMAATKETRENFANSAVEPTRKYGPDGVDDWEYFVPSGGLPCGNSR212
QY	152	-TDKQNYLALVRELKDAPEPHG-----YLLTAA--VSPGKDXIDRAYDIKLNKLFDMW202
Db	213	PEDKNNHLLLOQEVNDRKJDEAGQBDGKDYLLITASGASPGYVENNK---LNEIAEIVDWI269
QY	203	NWMTYDYHGGWENFYGHNAPLYKCPDETD-ELHT--YFNVNYTMHYLLANGATRDKLVMG259
Db	270	NIMTYDFGGWQNI SGHNAPLYDPATANTELPTPEHFNVESAVERGHLQAGVPEHKLVLG329
QY	260	VFPYGRANSIEDRSKLKLDPAKGWSPPGFISGEGVLSYIELCOLFOKEWHIQ---YD316
Db	330	MPFYGRGWSNCDEGA--NOGEYQR-CAPPREGTWENGVFDESFL-----EDHYINKNGVQ380
QY	317	EYVN---APYGN--DKIWIYDIDLASISCKLAPLKLGLVSGVWYMSLENDDFKHCPC370
Db	381	RWNOVAKVPFLYNATNGNFTYDDEBSFRKYTFIKSNMLASGMFWDVSGDR-----433
QY	371	KNPLLKNVHNMINGDERKNSFECILGPSTTPTTPTTPTTPTTPTTPTTPTTPTTPTT430
Db	434	-----NGTLLTALADQLG---FTPHEGOEPEEPSSAPTNIAQETVSTTWTLT478
QY	431	---PTTBSPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTT474
Db	479	WOAPTEBPTQYSAVYDSKEKTTHTTHTTIDLBQETTYTFVWSAEHKDGRHRAQALQVT538
QY	475	PKYTTVDG-----HLIKCYKEGD-IEBPTNINHILVCFBVGWVWHIMPBGPT---524
Db	539	TKSETGGDCTAPTQWANNVYTGDOVQHGGKLYE-----AKWWT--TGEBEPTTGB588
QY	525	--IW526
Db	589	WGWV592

RESULT 15
A38368
Chitinase (EC 3.2.1.14) precursor - Bacillus circulans
C/Species: Bacillus circulans
C/Date: 28-Jun-1991 #sequence_revision 28-Jun-1991 #text_change 15-Oct-1999
C/Accession: A38368
R/Matanabe, T.; Suzuki, K.; Oyanagi, W.; Ohnishi, K.; Tanaka, H.
J. Biol. Chem. 265, 15659-15663, 1990
A/TITLE: Gene cloning of chitinase A1 from Bacillus circulans WL-12 revealed its evolutionary relationship with chitinase A2 from Bacillus subtilis
A/Reference number: A38368; MUID: 90368776; PMID:2203782
A/Accession: A38368
A/Status: Preliminary
A/Molecule type: DNA
A/Residues: 1-699 <WAT>
A/Cross-references: GB:J05599; NID:gl06G341; PIDN:AAA81528.1; PID:gl42688
C/Superfamily: fibronectin type III repeat homology
C/Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 18.6%; Score 561; DB 2; Length 699;
Best Local Similarity 29.4%; Pred. No. 2.4e-27;
Matches 170; Conservative 67; Mismatches 185; Indels 156; Gaps 23;

[illegible]

```

103 NEKSQTINPNCITVLGDPHDIDTKTFAGTWDOPIAGNINQLNKLKQTNPNLKTIIISVG 166
QY 99 GMYEGSEKYSMDAANPTVROQFIOISVLDFOEQYKFDGLDLDWEYP--GSLGNPK--IDK 154
Db 163 GW--TWSNRFSDVAAATAATREVFANSAVDFLRKNYFDGVDLDWEYPVSGDGLGNSKEPEDK 221
QY 155 QNYLALVRELKDAFEPHG-----YLATAAVSPGKKDIDRAYDIDKELNKLFDMMNVTYD 208
Db 222 QNTLLSKIREKLDRAGAVDGKXYLLTIA--SGASATYAANTELAKIAAIVDMINIMTYD 280
QY 209 YHGGMENFYGHNAPLYKSPDET---DELHTYFNVNTYMHYLYNNGATRDKLVGVPFFYG 264
Db 281 FNGAWOKISAHNAPLYNDPAASAAGVPDANT--FNVAAGAOGHLDAGVPAKLVGLVGPFFYG 339
QY 265 RAWSIEDRSKLLGDPAGKMGPPGFISGEEGVLSVIELCOLFOKEWHIQ---YDSYIN-- 320
Db 340 RGMDCGACNGQYCTCTGGSGVG--TWEAGSFYIDL-----EANYINKGYYTYWND 391
QY 321 ---APYGN--DKIMVGYYDDLASISCKLAFELKELGVSVMVSLENDDPFGHCGRKPNLL 375
Db 392 TAKVPVLYNASNKRIFISYDDAESGVYKTAIYKSGLGGMFWELSGDRNK----- 441
QY 376 NKVHNMINGDEKNSFECILGPSTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPT 417
Db 442 -TLQNLKAD-----LPTGGTVPVVDTTAPSPVGNARSTGVANSVTLANW 486
QY 418 -----SPPTPTPTPTPTPTPTPT-----PSPTT 439
Db 487 ASDNVGVTVGVNYNGAMLAISVGTGTTATISGLTAGTSYFTTIKADAGNLGAASNAVT 546
QY 440 PTTTSP--TTPTPTPTP-APTSTSPSTTTTHTSET 474
Db 547 VSTTAQFGGDTOAPTAPTNLAATACTTSSITLSTWAST 584

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Search completed: March 22, 2004, 07:01:31
Job time : 35.8594 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 22, 2004, 06:42:54 ; Search time 43.2018 Seconds
(without alignments)
640.518 Million cell updates/sec

Title: US-09-662-293-21
Perfect score: 3014
Sequence: 1 SIKRDNDYSKNPRLVYCV.....IMPCPPGTWCOEKLTCIGE 536

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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2: /cgn2_6/prodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/prodata/2/iaa/5A_COMB.pep:*
4: /cgn2_6/prodata/2/iaa/5B_COMB.pep:*
5: /cgn2_6/prodata/2/iaa/5A_COMB.pep:*
6: /cgn2_6/prodata/2/iaa/5B_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3014	100.0	536	US-09-292-225-21	Sequence 21, Appl
2	3014	100.0	536	US-09-292-225-15	Sequence 15, Appl
3	3014	100.0	536	US-09-292-225-18	Sequence 18, Appl
4	2475	82.1	490	US-09-292-225-41	Sequence 41, Appl
5	2475	82.1	509	US-09-292-225-35	Sequence 35, Appl
6	2475	82.1	509	US-09-292-225-38	Sequence 38, Appl
7	834	27.7	554	US-08-524-051-2	Sequence 2, Appl
8	834	27.7	554	US-09-052-778-16	Sequence 16, Appl
9	812.5	27.0	583	US-09-545-814-2	Sequence 2, Appl
10	812.5	27.0	583	US-09-545-814-5	Sequence 5, Appl
11	811.5	26.9	559	US-09-545-814-14	Sequence 14, Appl
12	809.5	26.9	635	US-09-545-814-32	Sequence 32, Appl
13	738	24.5	466	US-08-486-839-4	Sequence 4, Appl
14	738	24.5	466	US-09-151-011-4	Sequence 4, Appl
15	738	24.5	466	US-09-039-198A-2	Sequence 2, Appl
16	738	24.5	466	US-09-343-623-4	Sequence 4, Appl
17	738	24.5	466	US-08-877-599-2	Sequence 2, Appl
18	738	24.5	466	US-09-367-574-2	Sequence 2, Appl
19	732.5	24.3	387	US-08-486-839-6	Sequence 6, Appl
20	732.5	24.3	387	US-09-151-011-6	Sequence 6, Appl
21	732.5	24.3	387	US-09-343-623-6	Sequence 6, Appl
22	732	24.3	466	US-09-039-198A-4	Sequence 4, Appl
23	732	24.3	466	US-08-877-599-4	Sequence 4, Appl
24	732	24.3	466	US-09-267-574-4	Sequence 4, Appl
25	721.5	23.9	373	US-09-039-198A-14	Sequence 14, Appl
26	721.5	23.9	373	US-09-039-198A-15	Sequence 15, Appl
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28	721.5	23.9	373	4	US-08-877-599-15	Sequence 15, Appl
29	721.5	23.9	373	4	US-09-267-574-14	Sequence 14, Appl
30	721.5	23.9	373	4	US-09-267-574-15	Sequence 15, Appl
31	672.5	22.3	489	4	US-09-545-814-29	Sequence 29, Appl
32	650	21.6	383	4	US-09-459-749D-17	Sequence 17, Appl
33	630	20.9	385	2	US-08-694-915-2	Sequence 2, Appl
34	630	20.9	416	2	US-08-694-915-4	Sequence 4, Appl
35	630	20.9	423	4	US-08-850-348A-2	Sequence 2, Appl
36	419.5	13.9	700	4	US-09-408-647A-2	Sequence 2, Appl
37	415	13.8	440	3	US-09-052-778-13	Sequence 13, Appl
38	411.5	13.7	442	3	US-09-052-778-2	Sequence 2, Appl
39	411	13.6	389	1	US-07-939-501A-1	Sequence 1, Appl
40	411	13.6	389	3	US-08-448-398-7	Sequence 7, Appl
41	411	13.6	423	1	US-07-939-501A-10	Sequence 10, Appl
42	411	13.6	423	1	US-07-939-501A-12	Sequence 12, Appl
43	403.5	13.4	561	1	US-08-358-901-2	Sequence 2, Appl
44	403.5	13.4	561	1	US-08-566-347-2	Sequence 2, Appl
45	403.5	13.4	561	1	US-08-693-835-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-09-292-225-21
; Sequence 21, Application US/09292225
; Patent No. 6455686
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/09/292,225
; CURRENT FILING DATE: 1999-04-15
; EARLIER APPLICATION NUMBER: 60/098,909
; EARLIER FILING DATE: 1998-09-02
; EARLIER APPLICATION NUMBER: 60/085,295
; EARLIER FILING DATE: 1998-05-13
; EARLIER APPLICATION NUMBER: 60/098,565
; EARLIER FILING DATE: 1998-04-17
; EARLIER APPLICATION NUMBER: 09/062,013
; EARLIER FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 536
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-09-292-225-21

Query Match	100.0%;	Score 3014;	DB 4;	Length 536;
Best Local Similarity	100.0%;	Pred. No. 1.2e-232;	Mismatches 0;	Indels 0;
Matches 536;	Conservative 0;			Gaps 0;
QY	1	SIKRDNDYSKNPRLVYCVGTWSYHKVDPTTIEDIDPFKCTHLMYGFAKIDYKTIQ	60	
Db	1	SIKRDNDYSKNPRLVYCVGTWSYHKVDPTTIEDIDPFKCTHLMYGFAKIDYKTIQ	60	
QY	61	VDPFDQDDNHSWEKRGYERFNRLKNPDLTWTISLGGWYEGSEKYSMDAANPTYROOF	120	
Db	61	VDPFDQDDNHSWEKRGYERFNRLKNPDLTWTISLGGWYEGSEKYSMDAANPTYROOF	120	
QY	121	TOSVLDFLOEYKFDGLDLDWEYVGSRLGNPKIDKQNYLALVRELKDAPEPHGYLLTAUVS	180	
Db	121	TOSVLDFLOEYKFDGLDLDWEYVGSRLGNPKIDKQNYLALVRELKDAPEPHGYLLTAUVS	180	
QY	181	PGKDKIDRAYDIKELNKLFDWNNVNTYDHGWFNFYGHNAFLYKRPDETDELHTYFNVN	240	
Db	181	PGKDKIDRAYDIKELNKLFDWNNVNTYDHGWFNFYGHNAFLYKRPDETDELHTYFNVN	240	
QY	241	YTMHYLLNNGATRDKLVMGVFFYGRAWSIEDRSKLKLGDPKAGMSPPGFISGEEGVLSYI	300	

Db 241 YTHYLLNNGATDKLVGVPFFYGRWSIEDRSKLGDPAGKMSPPGFISGEGVLSYI 300
Qy 301 ELCQLFQKEWHIOYDEYNAPYNDKIWGYDDLASISCKLAFKELGVSVMWSLE 360
Db 301 ELCQLFQKEWHIOYDEYNAPYNDKIWGYDDLASISCKLAFKELGVSVMWSLE 360
Qy 361 NDDFKHCGPKNPLNKHVNMINGDEKNSFECILGSPSTTTTPTTPTTPTTPTTPT 420
Db 361 NDDFKHCGPKNPLNKHVNMINGDEKNSFECILGSPSTTTTPTTPTTPTTPTTPT 420
Qy 421 TPTTPTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPT 480
Db 421 TPTTPTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPT 480
Qy 481 VDGHLLIKYKGGDIPHPNTIHKYLVCFFVNGWVHIMPCPPGTIWCQEKLTCTIGE 536
Db 481 VDGHLLIKYKGGDIPHPNTIHKYLVCFFVNGWVHIMPCPPGTIWCQEKLTCTIGE 536

RESULT 2
US-09-292-225-15
; Sequence 15, Application US/09292225
; Patent No. 6455686
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/09/292,225
; EARLIER FILING DATE: 1999-04-15
; EARLIER APPLICATION NUMBER: 60/098,909
; EARLIER FILING DATE: 1998-09-02
; EARLIER APPLICATION NUMBER: 60/085,295
; EARLIER FILING DATE: 1998-05-13
; EARLIER APPLICATION NUMBER: 60/098,565
; EARLIER FILING DATE: 1998-04-17
; EARLIER APPLICATION NUMBER: 09/062,013
; EARLIER FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 555
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-09-292-225-15

Query Match 100.0%; Score 3014; DB 4; Length 555;
Best Local Similarity 100.0%; Pred. No. 1.3e-232;
Matches 536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 20 SIKRDHNDYSKNPMRIVCYVGTWSVYHKVDPTYTIEDIDPFKTHLMYGAKEIDYKTYIQ 79
Qy 61 VFDPYQDDNHNSEKRGYERFNNLRKNPELTMTISLGGWYEGSEKYSMAANPTYRQOF 120
Db 80 VFDPYQDDNHNSEKRGYERFNNLRKNPELTMTISLGGWYEGSEKYSMAANPTYRQOF 139
Qy 121 IQSVLDFLOEYKFDGLDLDWEYPGSLGNPKIDKQNYLALVRELKDAFEPHGYLLTAAYS 180
Db 140 IQSVLDFLOEYKFDGLDLDWEYPGSLGNPKIDKQNYLALVRELKDAFEPHGYLLTAAYS 199
Qy 181 PGKDKIDRAYDIKELNKLFDWMNVMTYDHGWNENFYGHNAPLYKRPDETDELHLYFNVN 240
Db 200 PGKDKIDRAYDIKELNKLFDWMNVMTYDHGWNENFYGHNAPLYKRPDETDELHLYFNVN 259
Qy 241 YTHYLLNNGATDKLVGVPFFYGRWSIEDRSKLGDPAGKMSPPGFISGEGVLSYI 300
Db 260 YTHYLLNNGATDKLVGVPFFYGRWSIEDRSKLGDPAGKMSPPGFISGEGVLSYI 319

Qy 301 ELCQLFQKEWHIOYDEYNAPYNDKIWGYDDLASISCKLAFKELGVSVMWSLE 360
Db 320 ELCQLFQKEWHIOYDEYNAPYNDKIWGYDDLASISCKLAFKELGVSVMWSLE 379
Qy 361 NDDFKHCGPKNPLNKHVNMINGDEKNSFECILGSPSTTTTPTTPTTPTTPTTPT 420
Db 380 NDDFKHCGPKNPLNKHVNMINGDEKNSFECILGSPSTTTTPTTPTTPTTPTTPT 439
Qy 421 TPTTPTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPT 480
Db 440 TPTTPTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPT 499
Qy 481 VDGHLLIKYKGGDIPHPNTIHKYLVCFFVNGWVHIMPCPPGTIWCQEKLTCTIGE 536
Db 500 VDGHLLIKYKGGDIPHPNTIHKYLVCFFVNGWVHIMPCPPGTIWCQEKLTCTIGE 555

RESULT 3
US-09-292-225-18
; Sequence 18, Application US/09292225
; Patent No. 6455686
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/09/292,225
; EARLIER FILING DATE: 1999-04-15
; EARLIER APPLICATION NUMBER: 60/098,909
; EARLIER FILING DATE: 1998-09-02
; EARLIER APPLICATION NUMBER: 60/085,295
; EARLIER FILING DATE: 1998-05-13
; EARLIER APPLICATION NUMBER: 60/098,565
; EARLIER FILING DATE: 1998-04-17
; EARLIER APPLICATION NUMBER: 09/062,013
; EARLIER FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 555
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-09-292-225-18

Query Match 100.0%; Score 3014; DB 4; Length 555;
Best Local Similarity 100.0%; Pred. No. 1.3e-232;
Matches 536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SIKRDHNDYSKNPMRIVCYVGTWSVYHKVDPTYTIEDIDPFKTHLMYGAKEIDYKTYIQ 60
Db 20 SIKRDHNDYSKNPMRIVCYVGTWSVYHKVDPTYTIEDIDPFKTHLMYGAKEIDYKTYIQ 79
Qy 61 VFDPYQDDNHNSEKRGYERFNNLRKNPELTMTISLGGWYEGSEKYSMAANPTYRQOF 120
Db 80 VFDPYQDDNHNSEKRGYERFNNLRKNPELTMTISLGGWYEGSEKYSMAANPTYRQOF 139
Qy 121 IQSVLDFLOEYKFDGLDLDWEYPGSLGNPKIDKQNYLALVRELKDAFEPHGYLLTAAYS 180
Db 140 IQSVLDFLOEYKFDGLDLDWEYPGSLGNPKIDKQNYLALVRELKDAFEPHGYLLTAAYS 199
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Db 200 PGKDKIDRAYDIKELNKLFDWMNVMTYDHGWNENFYGHNAPLYKRPDETDELHLYFNVN 259
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Db 260 YTHYLLNNGATDKLVGVPFFYGRWSIEDRSKLGDPAGKMSPPGFISGEGVLSYI 319
Qy 301 ELCQLFQKEWHIOYDEYNAPYNDKIWGYDDLASISCKLAFKELGVSVMWSLE 360
Db 320 ELCQLFQKEWHIOYDEYNAPYNDKIWGYDDLASISCKLAFKELGVSVMWSLE 379


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Db      435  -----PITTDSTSEPKYTYID 432
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Db      453  GHLIKYKGGYLPHTDVHKYLVCEYIATPAGGWWVHIMDCPKGTRWHLTKNCIOE 509

RESULT 6
US-09-292-225--38
; Sequence 38, Application US/09292225
; Patent No. 6455686
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/09/292,225
; CURRENT FILING DATE: 1999-04-15
; EARLIER APPLICATION NUMBER: 60/098,909
; EARLIER FILING DATE: 1998-09-02
; EARLIER APPLICATION NUMBER: 60/085,295
; EARLIER FILING DATE: 1998-05-13
; EARLIER APPLICATION NUMBER: 60/098,565
; EARLIER FILING DATE: 1998-04-17
; EARLIER APPLICATION NUMBER: 09/062,013
; EARLIER FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 38
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-09-292-225-38

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Query Match	82.1%	Score	2475;	DB	4;	Length	509;
Best Local Similarity	82.5%;	Pred. No.	1.3e-189;				
Matches	443;	Conservative	21;	Mismatches	21;	Indels	52;
Gaps	2;						
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DB	22	KRDHNNYSKPMR	ITCVGVGWSVYHKVD	PPYTIEDIDDPFKCTHLMYGAKID	EYKTYIQVF	81	
QY	63	DPYODDNHNSWEKRGYERFNNLR	LKNPELITMISLGWYEGSEKYSDMAANPT	YRQOFIQ	122		
DB	82	DPFODDNHNSWEKRGYERFNNLR	LKNPELITMISLGWYEGSEKYSDMAANPT	YRQOFVQ	141		
QY	123	SVLDFLQEQKFDGLDLDWEY	PGSRIGNPKIDKQNYLALVRELKDAEP	PHGYLLTAAVSPG	182		
DB	142	SVLDFLQEQKFDGLDLDWEY	PGSRIGNPKIDKQNYLTLVRELKEAEP	PHFGYLLTAAVSPG	201		
QY	183	KDKIDRAYDIKELNKLFDMMVMY	TYHGGWENFYGHNAPLYKEP	DETDDELHTYFNNYT	242		
DB	202	KDKIDVAYELKELNQLFDMMVMY	TYHGGWENFYGHNAPLYKEP	DETDDELHTYFNNYT	261		
QY	243	MHYLLNNGATRDKLVMGVP	PYGRAWSTEDRSKILGDP	PAKMSPPGIFISGEEGLVSYIEL	302		
DB	262	MHYLLNNGATRDKLVMGVP	PYGRAWSIEDRSKVILGDP	PAKMSPPGIFITGEEGLVSYIEL	321		
QY	303	COLFQKEEWHIQDVEYNAPY	GYNDKILWGVDDLASISCKLAF	IKELGVSGVMWWSLEND	362		
DB	322	COLFQKEEWHIQDVEYNAPY	GYNDKILWGVDDLASISCKLAF	LKELGVSGVMWWSLEND	381		
QY	363	DFKGHCGRKPNLLKNVHNM	LNGEKNSEFCILGPSTTTPT	PTPTTTPTPTPTPTPTPT	422		
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QY 483 GHLIKCYKEGDIPIHPTNHIKVLCEYFV---NGWVHWIMPCPPGTIWQCEKLTCTIGE 536
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Db 453 GHLIKCYKQSYLPHTPDVHKVLVCEY:ATPNCGWVHWIMPCPKGTWHTATLKNCIQOE 509

RESULT 7
US-08-524-051-2
; Sequence 2, Application US/08524051
; Patent No. 5866788
; GENERAL INFORMATION:
; APPLICANT: Kramer, Karl J.
; APPLICANT: Muthukrishnan, Subbaratnam
; APPLICANT: Choi, Hee Kyung
; APPLICANT: Corpuz, Lolita
; APPLICANT: Gopalakrishnan, Bhuvana
; TITLE OF INVENTION: RECOMBINANT CHITINASE AND USE THEREOF AS
; TITLE OF INVENTION: A BIOCIDES
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hovey, Williams, Timmons & Collins
; STREET: 2405 Grand Blvd., Suite 400
; CITY: Kansas City
; STATE: MO
; COUNTRY: USA
; ZIP: 64108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/524,051
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Collins, John W.
; REGISTRATION NUMBER: 26,262
; REFERENCE/DOCKET NUMBER: 22875-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (816)474-9050
; TELEFAX: (816)474-9057
; TELEX: 434-383
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 554 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-524-051-2

Query Match 27.7%; Score 834; DB 2; Length 554;
Best Local Similarity 35.9%; Pred. No. 1.8e-58;
Matches 203; Conservative 76; Mismatches 202; Indels 84; Gaps 19;

QY 10 SKNPMRIVCYGVGWSVYHK-VDPYTTIEDIPFKCTHLMYGFADKIDEXYTIQVDPYQDD 68
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Db 19 SDSRARIVCYSNWAVYRPGVRYGIEDIPVEKCTHIYISYFIVGTGSEVLIIDPELD- 77
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QY 69 NNSWEKRGYERFNNLRKLNPELUTMISLGGWEGSEKYSMDAANPYRQOFISVLDLFL 128
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Db 78 ----VDKNQGRNFTSLRSSHPSKFWVAVGWAEAGSSKYSHWVAQKSTKSFIRSVVSL 133
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 129 QEYKFDGLDDWYBQSR-LGNPKIDQNYLALVRELKDAF--EPHGYLITAAVSPGDK 185
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Db 134 KYDFDGLDDWYBGAADRGSFSDKOKFLYLVQELRRAFIRVGKWEWLTAAVPLANFR 193
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 186 IDRAYDIKELNKLFDWNAVNTYHYHGWENFYHGNAPLYKRPDDELHTYFVNNYTMHY 245
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 194 LMESYHVPCLQELDAIHWSYDLRGWAGFADVHSELYKRPD-QWAYEKLNVNDGLHL 252
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 246 YLNGATRDKLNVGVFFYGSAMS:ED-----RSKLKLGDPKAGMSPPGFISGEE 294
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 253 WEEKGCPNSKLVVGIFFYGSFSLISAGNNNYGLTFINKRAGGDPAPYTNATGF----- 307
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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Db 478 HEEKSEQDNQVSGDATTATD---VDCSQEDYLPH-EDCNKYRC-----VHGEAV 525
 Qy 517 IMPCPPGTIW 526
 : : : : :
 Db 526 LFTCREGTV 535

 RESULT 10
 US-09-545-814-5
 ; Sequence 5, Application US/09545814
 ; Patent No. 6416977
 ; GENERAL INFORMATION:
 ; APPLICANT: Becher, Anna M.
 ; TITLE OF INVENTION: FLEA CHITINASE NUCLEIC ACID MOLECULES, PROTEINS AND
 ; TITLE OF INVENTION: FLEA CHITINASE NUCLEIC ACID MOLECULES, PROTEINS AND
 ; FILE REFERENCE: FC-5-C1
 ; CURRENT APPLICATION NUMBER: US/09/545,814
 ; CURRENT FILING DATE: 2000-04-07
 ; PRIOR APPLICATION NUMBER: 60/128,833
 ; PRIOR FILING DATE: 1999-04-09
 ; NUMBER OF SEQ ID NOS: 40
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 5
 ; LENGTH: 583
 ; TYPE: PRT
 ; ORGANISM: Ctenocephalides felis
 US-09-545-814-5

 Query Match 27.0%; Score 812.5; DB 4; Length 583;
 Best Local Similarity 35.6%; Pred. No. 1e-56;
 Matches 196; Conservative 86; Mismatches 197; Indels 71; Gaps 22

 Qy 10 SKNPMRIVCVGTWSVYHK-VDPYTIEDIDPFKCTHLMYGPAKIDEVKYTIQVDFPDQDD 68
 Db 24 SDQKARIVCFNNAVYRPGIRGYGIEDIPVDLCTHIVISFIVGDDKDKWSVLVIDPELDI 83
 Qy 69 NHNSWEKRGYERFNLRNLKPNELTTMI SLGGWYEGSKYSDMAANPYRQOFIQSVLDFL 128
 Db 84 DDN-----GPKNFTNLRKHPNVKQLIAGGWAEGGKKYSTWAEKRGAFIRSVVDPM 138
 Qy 129 QEYKFGDLDDWEYPGSR-LGNPKTIDKQNYLALVRLKDAFEPHG--YLTAAVSPGKK 185
 Db 139 NEYKFGDGLDWEYFGAADRGGSGDKDKFLYFVQELRRAPFNKQGNWEITMAVPIAKTR 198
 Qy 186 IDEAYDIDKLNKLPDMWVMTYDYHGGWENFVGHNAPLYKRPDETDELHTYFVNVYTMHY 245
 Db 199 LOEGYHVPELCELDAIHVMSYDLRGNWAGADTHSPLYRRPHD-QVAYEKLNVNDGLQL 257
 Qy 246 YLNGNATROKLVMPGPFYGRAWSIEDRSK-LKLG---DPAKGMSPPGFISGEEGVLSYIE 301
 Db 258 WVDNMGCPANKLVGVPPFYGRSTLNSNKDYELGTYNKEAGGEGEPGYTNATGPISYIE 317
 Qy 302 LCOLFO--KEEWHIQDEYNNAPYGYNDKIWGVYDDLASICKLAFKELGVSQVMVWSL 359
 Db 318 ICLEVDPSKGWTKWDEHGKVPYAYKGNQWGVYEDPKSVALKMEFIKSKGYGGAMTWA 377
 Qy 360 ENDDFFKGHG-PKNPLNKKVHNMINGDEKSFECILGSPSTTPP--TTPTPTPTPTPTPT 416
 Db 378 DMDDFGVCSDDKHTLATVIMHDYM---KNVIVPEFDSRITTPRFEWAKPSTPSQEP-D 432
 Qy 417 PSPTPTPT--TPSPT-TPPTTPSPSTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPT 469
 Db 433 DTPYIPTTAPSRKPTPKPKPT--TTTVAAATTPVAT-----TTTEHHHHH 477
 Qy 470 HTSETP-----KYTTYVDGHLIKCYKEGDIHPHTNIHKYLCBVFNGWVWVH---- 516
 Db 478 HEEKSEQDNQVSGDATTATD---VDCSQEDYLPH-EDCNKYRC-----VHGEAV 525
 Qy 517 IMPCPPGTIW 526
 Db 526 LFTCREGTV 535

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RESULT 11
US-09-545-814-14
; Sequence 14, Application US/09545814
; Patent No. 6416977
; GENERAL INFORMATION:
; APPLICANT: Becher, Anna M.
; TITLE OF INVENTION: FLEA CHITINASE NUCLEIC ACID MOLECULES, PROTEINS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCES: FC-5-C1
; CURRENT APPLICATION NUMBER: US/09/545,814
; CURRENT FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/128,833
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 559
; TYPE: PRT
; ORGANISM: Ctenocephalides felis
US-09-545-814-14

Query Match          26.9%   Score 811.5; DB 4; Length 559;
Best Local Similarity 35.8%; Pred. No. 1.1e-56;
Matches 195; Conservative 86; Mismatches 193; Indels 71; Gaps 22;

Qy      15 RIVCYGCTGWSYHK-VDPYTIETIDPKCTHLMYGFAKIDBYKTIQVDFYQDDNNHSW 73
Db      15 RIVCYFSPNWAYRPGICRYGIEDIPVDLCTHIVYVFGVDDKOWSLVIDFELDIDDN-- 62

Qy      74 EKGYERFNNLRINKPELTMTISLGGWYGESEKYSMDAANPTYEQQTQSVLDFLOEYKF 133
Db      74 ---GFKNFTNLRKTHPNVKLIQIAGVGAEGGKKYSTWVAEKKRSAPFIRSVVDPMYKF 119

Qy      134 DGLDLDWEYEGSR-LGNPKDKQNYLALVELKDAPEPHG--YLLTAAVSGPKDKIDRAY 190
Db      120 DGFDLDEYFCAADRGGSGFSDKOKFLYFVOELRFAFNKQGNWEITWAVP-IAPFLQEGY 179

Qy      191 DIKELNKLDFWMNVMTYDHYGGWENFYGHNAPLYKRDETDDELHTYFNVNVTMYVLLNG 250
Db      180 HVPCLCELLDAIHVMSYDLRGNWAGFADTHSPLVRRPHD-QAYEKLNVNDGLQLWDMVG 238

Qy      251 ATRDKLVMGVPFYGRAWSIEDRSK-LKLG---DPAKGMSPPGFISGEEGLSYIELCOLF 306
Db      239 CPANKLVGVPPFYGRSFTLSNSNKDYLRTGYINKEAGGEGPGPYTNATGFSYVEICLEV 298

Qy      307 Q--KEEWHIQVDEYNAPYGNDKIYVGYDDLAGISOKLAPLKELGVSQVMVWLENDDF 364
Db      299 DDPKSGWTKWDEHGKYPVAYKGNQWGVYEDPKSVALKMEFIKSGYGGAMTWAIDMDPF 358

Qy      365 XGHCG-PKNPLNKKVHNMINGDENKSECIILGPSTTTP--TTTPTPTPTTPTTPTPT 421
Db      359 QGVCSDDKHTLAVLMHDYM---KNYIVPFDSSRITPRPSWAKPPSTPSQEP-DDTPI 413

Qy      422 PTT-TPSPT-TPTTTPSPTPTTPPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPT 474
Db      414 PTHAPPSRKPTRKPKPT--TTTVAATTPVAT-----TTTEHHHHHHHEEK 458

Qy      475 P-----KYTTVVBGHLIKCYKEGDIPHTNIHKYLVCFYVNGGWVH-----IMCP 521
Db      459 PSEQDNQVGSQDTATD---VDCSQEDYLPH-EDCNKYRC-----VHGEAVLFCR 506

Qy      522 PGTW 526
Db      507 EGIVY 511

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RESULT 12
US-09-545-814-32
; Sequence 32, Application US/09545814
; Patent No. 6415977
; GENERAL INFORMATION:
; APPLICANT: Becher, Anna M.
; TITLE OF INVENTION: FLEA CHITINASE NUCLEIC ACID MOLECULES, PROTEINS AND


```

; TITLE OF INVENTION:  US THEREOF
; FILE REFERENCE:  FC-5-C1
; CURRENT APPLICATION NUMBER:  US/09/545,814
; CURRENT FILING DATE:  2000-04-07
; PRIOR APPLICATION NUMBER:  60/128,833
; PRIOR FILING DATE:  1999-04-09
; NUMBER OF SEQ ID NOS:  40
; SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 32
; LENGTH:  635
; TYPE:  PRT
; ORGANISM:  Tagged Ctenocephalides felis
; US-09-545-814-32

Query Match      26.9%; Score 809.5; DB 4; Length 635;
Best Local Similarity 35.6%; Pred. No. 2e-56;
Matches 196; Conservative 85; Mismatches 198; Indels 71; Gaps 22;

QY 10 SKNPMRIVCVGVWVSHK-VDPYTTIEDDPFKCTHLMYGFKAKIDKYKTYQVDFPQYD 68
DB 25 SDQKARIVCVFNSWAYRPGIGYGIEDIPVDLCTHIVVSFIGVDDKXMSVLVIDPDL 84
QY 69 NNSWKRGRYERFNNLRKNPELTWISLGGWYEGSEKSDMAANPTYQQTQISVLDPL 128
DB 85 DDN-----GPKNTNLKTHPNVKQLAVGWAEGGKYSTVMAEKRSAPFIRSVDPM 139
QY 129 QBYKFDGLDLDWYPSR-LGNPKIDKQNYLALVRELKDAFEPHG--YLLTAAVSPGDK 185
DB 140 NEYKFDGLDLDWYPSAADRGGSFSDKDFLYFVQELREAFNKGKQKWEITMAVPIAKFR 199
QY 186 IDRAYDIKELNKLFDWMNVTYDVGWENFYGHNAFLYKRPDETDELHTYFNVTMHY 245
DB 200 LQBGYHVPFELCELDLHVNYSYDLRGNWAGFATHSPLRYRPHD-QYAYEKLNVNDGLQ 258
QY 246 YLANGATRDKLVMGVPPYGRAMWIEDRSK-LKLQ----DPAKGMSPPGFISGEEGVLSTY 301
DB 259 WVDNGCPANKLVGVPPYGFPTLSNKNDRYLGTYINKEAGGEGPYTNATGFSIY 318
QY 302 LCQLFQ--KEEWHIOYDEYNAPYGYNDKTIWGYDDLASISCKLAFKELGVSGVMVWSL 359
DB 319 ICLEVDPSKGTWKWDEHKGVYAYKGNQWGVYEDPKSVALKWFNIKSGYGGAMTWA 378
QY 360 ENDDFKHCG-PKNPLLNKVNHNMGDEKNSFCILGPSTTTTP--TTTPTTPTTPTT 416
DB 379 DMDDFQVCSDRKHDLAVIMHDYN----KNYIVPEFDSRITRPEWAKFPSTPQEP-D 433
QY 417 PSPPTPTT-TPSPN-TPPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTT 469
DB 434 DTPYIPTHAPKPSRKTRPKPT--TTTVAATTPVAT-----TTTTHHHH 478
QY 470 HTSETP-----KYTTVVDGHLIKCYKEGDIPIPTNHLKYLVCBFVNGGWWVH---- 516
DB 479 HESEKPSQDNQVGSQDTATD---VDCSQEDYLPH-EDCNKYRC-----VHGEAV 526
QY 517 IMPCFPGTW 526
DB 527 LFTCREGTV 536

RESULT 13
US-08-486-839-4
; Sequence 4, Application US/08486839
; Patent No. 5928928
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION:  A human chitinase, its recombinant
; TITLE OF INVENTION:  production, its use for decomposing chitin, its use
; TITLE OF INVENTION:  in therapy or prophylaxis against infection diseases.
; NUMBER OF SEQUENCES:  16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE:  Hoffmann & Baron
; STREET:  350 Jericho Turnpike
; CITY:  Jericho

STATE:  New York
COUNTRY:  United States of America
ZIP:  11758
COMPUTER READABLE FORM:
MEDIUM TYPE:  Floppy disk
COMPUTER:  IBM PC compatible
OPERATING SYSTEM:  PC-DOS/MS-DOS
SOFTWARE:  PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER:  US/08/486,839
FILING DATE:  07 - June - 1995
ATTORNEY/AGENT INFORMATION:
NAME:  Baron, Ronald J.
REGISTRATION NUMBER:  29,281
REFERENCE/DOCKET NUMBER:  294-26
TELECOMMUNICATION INFORMATION:
TELEPHONE:  (516) 822-3550
TELEFAX:  (516) 822-3582
INFORMATION FOR SEQ ID NO:  4:
SEQUENCE CHARACTERISTICS:
LENGTH:  466 amino acids
TYPE:  amino acid
STRANDEDNESS:  unknown
TOPOLOGY:  unknown
MOLECULE TYPE:  protein
HYPOTHETICAL:  NO
US-08-486-839-4

Query Match      24.5%; Score 738; DB 2; Length 466;
Best Local Similarity 34.2%; Pred. No. 6.6e-51;
Matches 152; Conservative 85; Mismatches 150; Indels 58; Gaps 11;

QY 15 RIVCVGVWVSHKVDK-VYTTIEDDPFKCTHLMYGFKAKIDKYKTYQVDFPQYD 73
DB 23 KLVCFYTWQVYRQGEARFLPKDLPSLCTHLIYAFAGMTNHLST-----TEW 71
QY 74 -BKRGYEPNNLRKNPELTWISLGGWYEGSEKSDMAANPTYQQTQISVLDPLQYK 132
DB 72 NDETLQYEFNGLKKNPKLKTLLAIGGNWFGTQKFTDMVATANNRQTFVNSAIRFKYS 131
QY 133 FDGLDLDWYPSR-LGNPKIDKQNYLALVRELKDAFEPHG-----YLLTAAVSPGDK 185
DB 132 FDGLDLDWYPSQ-GSPAVDKERTTLVQDLANAFQEAOTSGKERLLLSAAVPAGTY 190
QY 186 IDRAYDIKELNKLFDWMNVTYDVGWENFYGHNAFLYKRPDETDELHTYFNVTMHY 245
DB 191 VDAGYEVNKLQNLDFVNLMAVDYFHGSWEKVTGHSNPLYKQESGAAS-LNVDAAVQQ 249
QY 246 YLANGATRDKLVMGVPPYGRAMWIEDRSKLGDPKGMSPPGFISGEEGVLSTYELCOL 305
DB 250 WLQKGTTPASKLILGMPTVGRSFTLASSSDTRVGPATGSGTGPPTKEGGLAYVEVGSW 309
QY 306 FQKEEWHIOYDEYNAPYGYNDKTIWGYDDLASISCKLAFKELGVSGVMVWSLEND 365
DB 310 KGATQRIQ-DQ--KVPYIFRDNQWGVDFDESFKTSYKQKGLGGMWALDLDFA 366
QY 366 GHCGPKNPLNKNVHNMGDEKNSFCILGPSTTTPTTPTTPTTPTTPTTPTTPTT 425
DB 367 G-----FSCNQG-----RYPLIQTLRQELSLVLPSTG 394
QY 426 PSPPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTT 450
DB 395 PELEVP-KEQQSEPEHGFSPGQDT 418

RESULT 14
US-09-151-011-4
; Sequence 4, Application US/09151011
; Patent No. 6057142
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION:  A Human Chitinase, Its Recombinant
```

TITLE OF INVENTION: Production, Its Use For Decomposing Chitin, Its Use in
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:

ADDRESSEE: Hoffmann & Baron, LLP
STREET: 6900 Jericho Turnpike
CITY: Syosset
STATE: New York
COUNTRY: United States of America
ZIP: 11791

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE:

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/151,011
FILING DATE: 10 - September - 1998
ATTORNEY/AGENT INFORMATION:

NAME: Morriss, Robert C.
REGISTRATION NUMBER: 42,910
REFERENCE/DOCKET NUMBER: 294-32 DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 822-3550
TELEFAX: (516) 822-3582

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 466 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
US-09-151-011-4

Query Match 24.5%; Score 738; DB 3; Length 466;

Best Local Similarity 34.2%; Pred. No. 6.6e-51;
Matches 152; Conservative 85; Mismatches 150; Indels 58; Gaps 11;

QY 15 RIVCVGTWVSVHKVDP-YTIEDDPFKCTHLMYGFPAKIDYKTYIQVDFDQDNNNSW 73
DB 23 KLVCYFTWVAQYQGEARFLPKDLDFSLCTHLIYAFAGMTHQLST-----TEW 71
QY 74 -EKRGYERFNNRLKGNPKIDKQNYLALVRELKDAEPHG-----YLLTAAPSCKDK 132
DB 72 NDETLQEFNGLKKNNPKLTLIAIGGNVFGTKFTDMVATANNRQTFVNSAIRFLKYS 131
QY 133 FDGLDLDWEYPGSRIGNPKIDKQNYLALVRELKDAEPHG-----YLLTAAPSCKDK 185
DB 132 FDGLDLDWEYPGSQ-GSPAVDKERFTTLVQDLANAFQQAQTSQGERLLLSAAVPAGQTY 190
QY 186 IDRAYDIKELNKLFDWNNVMTYDHGGWENFYGHNAPLYKRPDETDELHTYFNVNYTHY 245
DB 191 VDAGYEVNDKIAQNLDVFNLMAYDFHGSWEKVTGHNSPLYKQESGAAS-LNVDAAVQ 249
QY 246 YLNGATRDKLVGMVFPYGRAMSIEDRSKLGDPKAGMSPGFTSGEGVLSYIELCOL 305
DB 250 WLQKGTTPASKLILGMFTYGRSTFLASSSDTRVGAPATGSGTGPFTKEGGLMAYEVCW 309
QY 306 FQKEEWHIQDEYNNAPYGVNDKIWGYDDLASISCKLAFKELGCVGVMVWSLENDFFK 365
DB 310 KGATKQRIQ-DQ--KVPYIFRDNQWGVDFDVESFKTKVSYLKQKGLGAMWALDLDFA 366
QY 366 GHCGPKNPLLNKVNHNMGDEKNSFECILGSPSTTTTPTTPTTPTTPTTPTTPTTPTT 425
DB 367 G-----FSCNQ-----RYPLIQTLRQELSLPVLPSGT 394
QY 426 PSPTPTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTT 450
DB 395 PELEVP-KFGQSEPEHGSPGQDT 418

RESULT 15

US-09-039-198A-2
Sequence 2, Application US/09039198A
Patent No. 6200951

GENERAL INFORMATION:
APPLICANT: Gray, Patrick W.
APPLICANT: Tjoelker, Larry W.
TITLE OF INVENTION: CHITINASE CHITIN-BINDING FRAGMENTS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive/6300 Sears Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/039,198A
FILING DATE:

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 27866/34391
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 466 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-039-198A-2

Query Match 24.5%; Score 738; DB 3; Length 466;

Best Local Similarity 34.2%; Pred. No. 6.6e-51;
Matches 152; Conservative 85; Mismatches 150; Indels 58; Gaps 11;

QY 15 RIVCVGTWVSVHKVDP-YTIEDDPFKCTHLMYGFPAKIDYKTYIQVDFDQDNNNSW 73
DB 23 KLVCYFTWVAQYQGEARFLPKDLDFSLCTHLIYAFAGMTHQLST-----TEW 71
QY 74 -EKRGYERFNNRLKGNPKIDKQNYLALVRELKDAEPHG-----YLLTAAPSCKDK 132
DB 72 NDETLQEFNGLKKNNPKLTLIAIGGNVFGTKFTDMVATANNRQTFVNSAIRFLKYS 131
QY 133 FDGLDLDWEYPGSRIGNPKIDKQNYLALVRELKDAEPHG-----YLLTAAPSCKDK 185
DB 132 FDGLDLDWEYPGSQ-GSPAVDKERFTTLVQDLANAFQQAQTSQGERLLLSAAVPAGQTY 190
QY 186 IDRAYDIKELNKLFDWNNVMTYDHGGWENFYGHNAPLYKRPDETDELHTYFNVNYTHY 245
DB 191 VDAGYEVNDKIAQNLDVFNLMAYDFHGSWEKVTGHNSPLYKQESGAAS-LNVDAAVQ 249
QY 246 YLNGATRDKLVGMVFPYGRAMSIEDRSKLGDPKAGMSPGFTSGEGVLSYIELCOL 305
DB 250 WLQKGTTPASKLILGMFTYGRSTFLASSSDTRVGAPATGSGTGPFTKEGGLMAYEVCW 309
QY 306 FQKEEWHIQDEYNNAPYGVNDKIWGYDDLASISCKLAFKELGCVGVMVWSLENDFFK 365
DB 310 KGATKQRIQ-DQ--KVPYIFRDNQWGVDFDVESFKTKVSYLKQKGLGAMWALDLDFA 366
QY 366 GHCGPKNPLLNKVNHNMGDEKNSFECILGSPSTTTTPTTPTTPTTPTTPTTPTTPTT 425
DB 367 G-----FSCNQ-----RYPLIQTLRQELSLPVLPSGT 394
QY 426 PSPTPTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTT 450

Db 395 PELEVP-KFGQFSEPHGSPGQDT 418

Search completed: March 22, 2004, 07:04:01
Job time : 44.2018 secs

Sequence 15, Appl
Sequence 14, Appl
Sequence 15, Appl
Sequence 29, Appl
Sequence 17, Appl
Sequence 2, Appl
Sequence 4, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 13, Appl
Sequence 10, Appl
Sequence 12, Appl
Sequence 1, Appl
Sequence 7, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 2, Appl

ALIGNMENTS

RESULT 1
 US-09-292-222-15
 ; Sequence 15, Application US/09292225
 ; Patent No. 6455686
 ; GENERAL INFORMATION:
 ; APPLICANT: McCall, Catherine A.
 ; APPLICANT: Hunter, Shirley Wu
 ; APPLICANT: Weber, Eric R.
 ; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
 ; TITLE OF INVENTION: AND USES THEREOF
 ; FILE REFERENCE: AU-2-C3
 ; CURRENT APPLICATION NUMBER: US/09/292,225
 ; CURRENT FILING DATE: 1999-04-15
 ; EARLIER APPLICATION NUMBER: 60/098,909
 ; EARLIER FILING DATE: 1998-09-02
 ; EARLIER APPLICATION NUMBER: 60/085,295
 ; EARLIER FILING DATE: 1998-05-13
 ; EARLIER APPLICATION NUMBER: 60/098,565
 ; EARLIER FILING DATE: 1998-04-17
 ; EARLIER APPLICATION NUMBER: 09/062,013
 ; EARLIER FILING DATE: 1998-04-17
 ; NUMBER OF SEQ ID NOS: 49
 ; SOFTWARE: PatentIn Ver. 2.0

Query Match	100.0%;	Score 3107;	DB 4;	Length 555;
Best Local Similarity	100.0%;	Pred. No. 6.5e-241;		
Matches 555:	Conservative	0:	Mismatches 0:	Indels 0:
	Gaps	0:		

[illegible]

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 22, 2004, 06:42:54 ; Search time 44.7332 Seconds
(without alignments) 640.518 Million cell updates

Title: US-09-662-293-18
 Perfect score: 3107
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

1977 JAN 24

Database : Issued Patents AA:*

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3: /cgn2_6/prodata/2/1aa/6A_COMB.per.*
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4: /cgn2_6/ptodata/2/1aa/6b COMB.per: *
5: /cgn2_6/ptodata/2/1aa/ptotus COMB.per: *
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6: /cgn2_6/ptodata/2/1aa/backrilles1.pbp:

pred. No. is the number of results predicted by char-

and is derived by analysis of the total score distribution

SUMMARIES

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100	100

[illegible]

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4	2542	81.8	509	4	US-09-292-225-35
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6	2475	79.7	490	4	US-09-292-225-41
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8	838.5	27.0	554	3	US-09-052-778-16
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10	815.5	26.2	583	4	US-09-545-814-5
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12.	811.5	26.1	559	4	US-09-545-814-14
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14	738	23.8	466	3	US-09-151-011-4
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16	738	23.8	466	4	US-09-343-623-4
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18	738	23.8	466	4	US-09-267-574-2
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20	732.5	23.6	387	3	US-09-151-011-6
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22	732	23.6	466	3	US-09-039-198A-4
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24	732	23.6	466	4	US-09-267-574-4
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26	721.5	23.2	373	3	US-09-039-198A-15
----	-------	------	-----	---	-------------------

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	3107	100.0	555	4	US-09-292-223-15	Sequence 15, Appl
2	3107	100.0	555	4	US-09-292-223-18	Sequence 18, Appl
3	3014	97.0	536	4	US-09-292-223-21	Sequence 21, Appl
4	2542	81.8	509	4	US-09-292-223-35	Sequence 35, Appl
5	2542	81.8	509	4	US-09-292-223-38	Sequence 38, Appl
6	2475	79.7	490	4	US-09-292-225-41	Sequence 41, Appl
7	838.5	27.0	554	2	US-08-524-051-2	Sequence 2, Appl
8	838.5	27.0	554	3	US-09-052-778-16	Sequence 16, Appl
9	815.5	26.2	583	4	US-09-545-814-2	Sequence 2, Appl
10	815.5	26.2	583	4	US-09-545-814-5	Sequence 5, Appl
11	812.5	26.2	635	4	US-09-545-814-32	Sequence 32, Appl
12	811.5	26.1	559	4	US-09-545-814-14	Sequence 14, Appl
13	738	23.8	466	2	US-08-486-833-4	Sequence 4, Appl
14	738	23.8	466	3	US-09-151-011-4	Sequence 4, Appl
15	738	23.8	466	3	US-09-039-198A-2	Sequence 2, Appl
16	738	23.8	466	4	US-09-343-623-4	Sequence 4, Appl
17	738	23.8	466	4	US-08-877-599-2	Sequence 2, Appl
18	738	23.8	466	4	US-09-267-574-2	Sequence 2, Appl
19	732.5	23.6	387	2	US-08-486-839-6	Sequence 6, Appl
20	732.5	23.6	387	3	US-09-151-011-6	Sequence 6, Appl
21	732.5	23.6	387	4	US-09-343-623-6	Sequence 6, Appl
22	732	23.6	466	3	US-09-039-198A-4	Sequence 4, Appl
23	732	23.6	466	4	US-08-877-599-4	Sequence 4, Appl
24	732	23.6	466	4	US-09-267-574-4	Sequence 4, Appl
25	721.5	23.2	373	3	US-09-039-198A-14	Sequence 14, Appl
26	721.5	23.2	373	3	US-09-039-198A-15	Sequence 15, Appl
27	731.5	23.2	373	4	US-08-877-599-14	Sequence 14, Appl

Db 241 PLYKRPDDELTHTYFNVNVTMHHYLLNNGATRDKLVGVFPFYGRAWSIEDRSKILGDPA 300
QY 301 KMSPPGFIISGEGVLSYIELCOLFOKEEWHIOYDEYNNAPYNDKIWGVYDDLASISC 360
Db 301 KMSPPGFIISGEGVLSYIELCOLFOKEEWHIOYDEYNNAPYNDKIWGVYDDLASISC 360
QY 361 KLAFLKELGSGVMVWSLENDDFKGGCHGPKNPLLNKVNHNMGDEKNSFECILGSPSTTP 420
Db 361 KLAFLKELGSGVMVWSLENDDFKGGCHGPKNPLLNKVNHNMGDEKNSFECILGSPSTTP 420
QY 421 TPPTTPT 480
Db 421 TPPTTPT 480
QY 481 TPSPTTTEHTSETPKYTYVDGHLIKCYKEGDIHPHTNIHKYLVCFVNGVWVHIMPCP 540
Db 481 TPSPTTTEHTSETPKYTYVDGHLIKCYKEGDIHPHTNIHKYLVCFVNGVWVHIMPCP 540
QY 541 PGTIWCQEKLTICIG 555
Db 541 PGTIWCQEKLTICIG 555

RESULT 2

US-09-292-225-18
; Sequence 18, Application US/09292225
; Patent No. 6455686
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/09/292,225
; CURRENT FILING DATE: 1999-04-15
; EARLIER APPLICATION NUMBER: 60/098,909
; EARLIER FILING DATE: 1998-09-02
; EARLIER APPLICATION NUMBER: 60/085,295
; EARLIER FILING DATE: 1998-05-13
; EARLIER APPLICATION NUMBER: 60/098,565
; EARLIER FILING DATE: 1998-04-17
; EARLIER APPLICATION NUMBER: 09/062,013
; EARLIER FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 18
; LENGTH: 555
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-09-292-225-18

Query Match 100.0%; Score 3107; DB 4; Length 555;
Best Local Similarity 100.0%; Pred. No. 6.5e-241;
Matches 555; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKTIYAILSIWACIGLNNASIKRDHNDYSKNPMRIVCYGTWSVYHKVDYTTIEDIDPPK 60
Db 1 MKTIYAILSIWACIGLNNASIKRDHNDYSKNPMRIVCYGTWSVYHKVDYTTIEDIDPPK 60
QY 61 CTHLMYGFAKIDEYKTYIQVDFPDYQDDNHNWSEKRGYERFNNLRLKNPELTTMISLGGWY 120
Db 61 CTHLMYGFAKIDEYKTYIQVDFPDYQDDNHNWSEKRGYERFNNLRLKNPELTTMISLGGWY 120
QY 121 EGSEKYSMDMAANPTYRQOFIQSVLDFLOEYKFDGLDWEYPSRGLGNPKIDKQNYALV 180
Db 121 EGSEKYSMDMAANPTYRQOFIQSVLDFLOEYKFDGLDWEYPSRGLGNPKIDKQNYALV 180
QY 181 RELKDAPEPHGYLLTAAVSPGCKIDRAYDIKELNKLFDWNNVTYDYGHWENFYGHNA 240
Db 181 RELKDAPEPHGYLLTAAVSPGCKIDRAYDIKELNKLFDWNNVTYDYGHWENFYGHNA 240

QY 241 PLYKRPDDELTHTYFNVNVTMHHYLLNNGATRDKLVGVFPFYGRAWSIEDRSKILGDPA 300
Db 241 PLYKRPDDELTHTYFNVNVTMHHYLLNNGATRDKLVGVFPFYGRAWSIEDRSKILGDPA 300
QY 301 KMSPPGFIISGEGVLSYIELCOLFOKEEWHIOYDEYNNAPYNDKIWGVYDDLASISC 360
Db 301 KMSPPGFIISGEGVLSYIELCOLFOKEEWHIOYDEYNNAPYNDKIWGVYDDLASISC 360
QY 361 KLAFLKELGSGVMVWSLENDDFKGGCHGPKNPLLNKVNHNMGDEKNSFECILGSPSTTP 420
Db 361 KLAFLKELGSGVMVWSLENDDFKGGCHGPKNPLLNKVNHNMGDEKNSFECILGSPSTTP 420
QY 421 TPPTTPT 480
Db 421 TPPTTPT 480
QY 481 TPSPTTTEHTSETPKYTYVDGHLIKCYKEGDIHPHTNIHKYLVCFVNGVWVHIMPCP 540
Db 481 TPSPTTTEHTSETPKYTYVDGHLIKCYKEGDIHPHTNIHKYLVCFVNGVWVHIMPCP 540
QY 541 PGTIWCQEKLTICIG 555
Db 541 PGTIWCQEKLTICIG 555

RESULT 3

US-09-292-225-21
; Sequence 21, Application US/09292225
; Patent No. 6455686
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/09/292,225
; CURRENT FILING DATE: 1999-04-15
; EARLIER APPLICATION NUMBER: 60/098,909
; EARLIER FILING DATE: 1998-09-02
; EARLIER APPLICATION NUMBER: 60/085,295
; EARLIER FILING DATE: 1998-05-13
; EARLIER APPLICATION NUMBER: 60/098,565
; EARLIER FILING DATE: 1998-04-17
; EARLIER APPLICATION NUMBER: 09/062,013
; EARLIER FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 21
; LENGTH: 536
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-09-292-225-21

Query Match 97.0%; Score 3014; DB 4; Length 536;
Best Local Similarity 100.0%; Pred. No. 1.8e-233;
Matches 536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 20 SIKRDHNDYSKNPMRIVCYGTWSVYHKVDYTTIEDIDPPKCTHLMYGFAKIDEYKTYIQ 79
Db 1 SIKRDHNDYSKNPMRIVCYGTWSVYHKVDYTTIEDIDPPKCTHLMYGFAKIDEYKTYIQ 60
QY 80 VFDPYQDDNHNWSEKRGYERFNNLRLKNPELTTMISLGGWYEGSEKYSMDMAANPTYRQOF 139
Db 61 VFDPYQDDNHNWSEKRGYERFNNLRLKNPELTTMISLGGWYEGSEKYSMDMAANPTYRQOF 120
QY 140 IQSVLDFLOEYKFDGLDWEYPSRGLGNPKIDKQNYALVRELKDAPEPHGYLLTAAVS 199
Db 121 IQSVLDFLOEYKFDGLDWEYPSRGLGNPKIDKQNYALVRELKDAPEPHGYLLTAAVS 180
QY 200 PGCKIDRAYDIKELNKLFDWNNVTYDYGHWENFYGHNAPLYKRPDDELTHTYFNVN 259
Db 181 PGCKIDRAYDIKELNKLFDWNNVTYDYGHWENFYGHNAPLYKRPDDELTHTYFNVN 240

Db 241 PLYKRDDELDHTYFNVNYTHYYLNNGATRDKLVNGVFFYGRAWSIEDRSKVLGDPGA 300
QY 301 KGMSPGFTGEGVLSYIELCOLFOKEBWHIOYDEYNNAPYCYNDKIWVGDDDLASISC 360
Db 301 KGMSPGFTGEGVLSYIELCOLFOKEBWHIOYDEYNNAPYCYNDKIWVGDDDLASISC 360
QY 361 KLAFLKELGVSGVWVWLSLNDPKHCGKPNPLNKNVHNMINGDEKNSPECILGSPSTTP 420
Db 361 KLAFLKELGVSGVWVWLSLNDPKHCGKPNPLNKNVHNMINGDEKNSPECILGSPSTTP 420
QY 421 TPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTT 480
Db 421 TPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTT 434
QY 481 TPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTT 537
Db 435 ---PTTDTSTPTKTYTIDGHLIKCYKQGLPHTDVKHLYVCEYATFNGGWWHIM 491
QY 538 PDPGPIWQCKLTCIGR 555
Db 492 DCPKGTREHATLKNICQE 509

RESULT 6
US-09-292-225-41
; Sequence 41, Application US/09292225
; Patent No. 6455686
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/09/292,225
; CURRENT FILING DATE: 1999-04-15
; EARLIER APPLICATION NUMBER: 60/098,909
; EARLIER FILING DATE: 1998-09-02
; EARLIER APPLICATION NUMBER: 60/085,295
; EARLIER FILING DATE: 1998-05-13
; EARLIER APPLICATION NUMBER: 60/098,565
; EARLIER FILING DATE: 1998-04-17
; EARLIER APPLICATION NUMBER: 09/062,013
; EARLIER FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 41
; LENGTH: 490
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-09-292-225-41

Query Match 79.7%; Score 2475; DB 4; Length 490;
Best Local Similarity 82.5%; Pred. No. 2.5e-190;
Matches 443; Conservative 21; Mismatches 21; Indels 52; Gaps 2;
QY 22 KRDHNSKNPRLVYCVGTWVSHKVDYTTIEDIDPKCTHLMYGFADIKYKTIQVF 81
Db 3 KRDHNSKNPRLVYCVGTWVSHKVDYTTIEDIDPKCTHLMYGFADIKYKTIQVF 62
QY 82 DPYQDNHNSWEKRGVERNNRLKNPELTMTISLGGWYEGSEKYSDMAANPTTRQIQ 141
Db 63 DPFQDNHNSWEKRGVERNNRLKNPELTMTISLGGWYEGSEKYSDMAANPTTRQIQ 122
QY 142 SVLDFLOEYKFGDLDDWYPSGRGNPKIDKONYLALVRLKDAFEHGYLLTAASPG 201
Db 123 SVLDFLOEYKFGDLDDWYPSGRGNPKIDKONYLALVRLKDAFEHGYLLTAASPG 182
QY 202 KDKIDRAYDINKELNKLFDWNNVNTYDYGWENFYNCHNAPLYKRPDETDLHTFNNVNT 261
Db 183 KDKIDVAYELKELNQLFDWNNVNTYDYGWENFYNCHNAPLYKRPDETDLHTFNNVNT 242

QY 262 MHYLNNGATRDKLVNGVFFYGRAWSIEDRSKVLGDPKMGSPPGFISGEGVLSYIEL 321
Db 243 MHYLNNGATRDKLVNGVFFYGRAWSIEDRSKVLGDPKMGSPPGFISGEGVLSYIEL 302
QY 322 COLFOKEBWHIOYDEYNNAPYCYNDKIWVGDDDLASISCKLAFKELGVSGVWVWLSLND 381
Db 303 COLFOKEBWHIOYDEYNNAPYCYNDKIWVGDDDLASISCKLAFKELGVSGVWVWLSLND 362
QY 382 DFKHCGKPNPLNKNVHNMINGDEKNSPECILGSPSTTPTTPTTPTTPTTPTTPTTPTT 441
Db 363 DFKHCGKPNPLNKNVHNMINGDEKNSPECILGSPSTTPTTPTTPTTPTTPTTPTTPTT 415
QY 442 TPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTT 501
Db 416 ---PTTDTSTPTKTYTID 433
QY 502 GHLIKCYKQGLPHTDVKHLYVCEYATFNGGWWHIMCPGPTIWCQKLTICIGR 555
Db 434 GHLIKCYKQGLPHTDVKHLYVCEYATFNGGWWHIMCPGPTIWCQKLTICIGR 490

RESULT 7
US-08-524-051-2
; Sequence 2, Application US/08524051
; Patent No. 5866788
; GENERAL INFORMATION:
; APPLICANT: Kramer, Karl J.
; APPLICANT: Muthukrishnan, Subbaratnam
; APPLICANT: Choi, Hee Kyung
; APPLICANT: Corpuz, Lolita
; APPLICANT: Gopalakrishnan, Bhuvana
; TITLE OF INVENTION: RECOMBINANT CHITINASE AND USE THEREOF AS
; TITLE OF INVENTION: A BIOCIDES
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hovey, Williams, Timmons & Collins
; STREET: 2405 Grand Blvd., Suite 400
; CITY: Kansas City
; STATE: MO
; COUNTRY: USA
; ZIP: 64108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/524,051
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Collins, John M.
; REGISTRATION NUMBER: 26,262
; REFERENCE/DOCKET NUMBER: 22875-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (816)474-9050
; TELEFAX: (816)474-9057
; TELEX: 434-363
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 554 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-524-051-2

Query Match 27.0%; Score 838.5; DB 2; Length 554;
Best Local Similarity 35.4%; Pred. No. 4.8e-59;
Matches 208; Conservative 79; Mismatches 210; Indels 91; Gaps 20;
QY 6 ALLSIMACIGLMMASIKRDHNSKPMRIVCVGTWVSHK-VDPYTTIEDIDPKCTH 64
Db 3 ATLATLAVLATAV-----QSDSRARIVCYFNWAVRPGVGRYGIEDIPVEKCTHI 55

Db 237 YRRPHD-QYAYEKLNVNDGLQLWDMGCPANKLVGVFPYGRSFTLSNSKDYRLGTIN 295
Qy 299 PAKGMSPPGFSIGBEGVLSYIELCOLFQ--KEEMHIQYDEYNAPYNDKIKWGYDDLA 356
Db 296 KEAGGREGPYTNATGFSYVEICLEVDPSKGTWKWDHKGKVPYAYKGNQWGYEDPK 355
Qy 357 SISCKLAFKELGVSGVMVNSLENDDFKGGCG-PKNPLLNKVNMMINGDEKNSFECILGP 415
Db 356 SVALKMEFIKSKGYGAMTWAIDMDDFGVCSDDKHTLAVIMHDYM---KNYIVPEFDS 411
Qy 416 STTTPTP--TTTPTPTPTPTPTPTPT--TPSPT--TPPTPTPTPTPTPTPTPTPTPT 471
Db 412 SRIIPREWAKPPSPSQEP-DDTPYIPTTHAPKPSRKPKPT--TTTVAATPVAT 468
Qy 472 TPTPAPTSTPSPTTTE-----HTSETP-----KYTTVDGHLIKCYKEGDIPHPT 517
Db 469 -----TTTEHHHHHEEKEPSEQDNQVGSQDTATD---VDCSQEDYLPH-E 511
Qy 518 NIHXYLVCBFVNGMWVH-----IMPCPPGTIW 545
Db 512 DCKNYRC-----VHGEAVLFTCREGTVY 535

RESULT 10
US-09-545-814-5
; Sequence 5, Application US/09545814
; Patent No. 6416977
; GENERAL INFORMATION:
; APPLICANT: Becher, Anna M.
; TITLE OF INVENTION: FLEA CHITINASE NUCLEIC ACID MOLECULES, PROTEINS AND
; FILE REFERENCE: FC-5-C1
; CURRENT APPLICATION NUMBER: US/09/545,814
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/128,833
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 5
; LENGTH: 583
; TYPE: PRT
; ORGANISM: Ctenocephalides felis
US-09-545-814-5

Query Match 26.2%; Score 815.5; DB 4; Length 583;
Best Local Similarity 34.6%; Pred. No. 3.6e-57;
Matches 198; Conservative 94; Mismatches 205; Indels 75; Gaps 23;
Qy 7 ILSIMACIGLMNASIKRDNDYKSNPMRIVCVVGTWSVYHK-VDPYTTIEDIDPFKCTHLM 65
Db 6 LLAVLCAIAISSINTV-----EASDQKARIVCVFSNVAVRPGIRYGIEDIPVDLCTHIV 61
Qy 66 YGFAKIDYKYTIQVDPYQDNNHNSWEKRGVERFNNLRKNPELTTMISLGWYEGSEK 125
Db 62 YSFIGVDDKWSVLVIDPELDIDDN-----GFKNFTNLKRIHPNVKLQIAGVGAEGGKK 116
Qy 126 YSDMAANTPYQQFOSVLDLQYKFDGLDWEYPGSR-LGNPKIDKQNYLALVRELK 184
Db 117 YSTMVAEKRSKSAFIRSVVDFMNEYKFDGLDWEYPGAADRGGSFSDKDKFLYFVQELR 176
Qy 185 DAFEPHG--YLLTAASPGKDKIDRAYDIKELNKLFDMMVNTYDYGWENFYGHNAFL 242
Db 177 RAFNKGKQWEITWAVPIAKFRLQEGYHVPCLCELLDAIHVMSYDLRGNWAGFADTHSPL 236
Qy 243 YKRPDDELTHYFNNTMYYLNGATRDKLVMGVPPYGRAWSIEDRSK-LKLG---D 298
Db 237 YRRPHD-QYAYEKLNVNDGLQLWDMGCPANKLVGVFPYGRSFTLSNSKDYRLGTIN 295
Qy 299 PAKGMSPPGFSIGBEGVLSYIELCOLFQ--KEEMHIQYDEYNAPYNDKIKWGYDDLA 356
Db 296 KEAGGREGPYTNATGFSYVEICLEVDPSKGTWKWDHKGKVPYAYKGNQWGYEDPK 355
Qy 357 SISCKLAFKELGVSGVMVNSLENDDFKGGCG-PKNPLLNKVNMMINGDEKNSFECILGP 415

Db 356 SVALKMEFIKSKGYGAMTWAIDMDDFGVCSDDKHTLAVIMHDYM---KNYIVPEFDS 411
Qy 416 STTTPTP--TTTPTPTPTPTPTPTPT--TPSPT--TPPTPTPTPTPTPTPTPTPTPT 471
Db 412 SRIIPREWAKPPSPSQEP-DDTPYIPTTHAPKPSRKPKPT--TTTVAATPVAT 468
Qy 472 TPTPAPTSTPSPTTTE-----HTSETP-----KYTTVDGHLIKCYKEGDIPHPT 517
Db 469 -----TTTEHHHHHEEKEPSEQDNQVGSQDTATD---VDCSQEDYLPH-E 511
Qy 518 NIHXYLVCBFVNGMWVH-----IMPCPPGTIW 545
Db 512 DCKNYRC-----VHGEAVLFTCREGTVY 535

RESULT 11
US-09-545-814-32
; Sequence 32, Application US/09545814
; Patent No. 6416977
; GENERAL INFORMATION:
; APPLICANT: Becher, Anna M.
; TITLE OF INVENTION: FLEA CHITINASE NUCLEIC ACID MOLECULES, PROTEINS AND
; FILE REFERENCE: FC-5-C1
; CURRENT APPLICATION NUMBER: US/09/545,814
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/128,833
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 32
; LENGTH: 635
; TYPE: PRT
; ORGANISM: Tagged Ctenocephalides felis
US-09-545-814-32

Query Match 26.2%; Score 812.5; DB 4; Length 635;
Best Local Similarity 34.6%; Pred. No. 7e-57;
Matches 198; Conservative 93; Mismatches 206; Indels 75; Gaps 23;
Qy 7 ILSIMACIGLMNASIKRDNDYKSNPMRIVCVVGTWSVYHK-VDPYTTIEDIDPFKCTHLM 65
Db 7 LLAVLCAIAISSINTV-----EASDQKARIVCVFSNVAVRPGIRYGIEDIPVDLCTHIV 62
Qy 66 YGFAKIDYKYTIQVDPYQDNNHNSWEKRGVERFNNLRKNPELTTMISLGWYEGSEK 125
Db 63 YSFIGVDDKWSVLVIDPELDIDDN-----GFKNFTNLKRIHPNVKLQIAGVGAEGGKK 117
Qy 126 YSDMAANTPYQQFOSVLDLQYKFDGLDWEYPGSR-LGNPKIDKQNYLALVRELK 184
Db 118 YSTMVAEKRSKSAFIRSVVDFMNEYKFDGLDWEYPGAADRGGSFSDKDKFLYFVQELR 177
Qy 185 DAFEPHG--YLLTAASPGKDKIDRAYDIKELNKLFDMMVNTYDYGWENFYGHNAFL 242
Db 178 RAFNKGKQWEITWAVPIAKFRLQEGYHVPCLCELLDAIHVMSYDLRGNWAGFADTHSPL 237
Qy 243 YKRPDDELTHYFNNTMYYLNGATRDKLVMGVPPYGRAWSIEDRSK-LKLG---D 298
Db 238 YRRPHD-QYAYEKLNVNDGLQLWDMGCPANKLVGVFPYGRFPTLSNSKDYRLGTIN 296
Qy 299 PAKGMSPPGFSIGBEGVLSYIELCOLFQ--KEEMHIQYDEYNAPYNDKIKWGYDDLA 356
Db 297 KEAGGREGPYTNATGFSYVEICLEVDPSKGTWKWDHKGKVPYAYKGNQWGYEDPK 356
Qy 357 SISCKLAFKELGVSGVMVNSLENDDFKGGCG-PKNPLLNKVNMMINGDEKNSFECILGP 415
Db 357 SVALKMEFIKSKGYGAMTWAIDMDDFGVCSDDKHTLAVIMHDYM---KNYIVPEFDS 412
Qy 416 STTTPTP--TTTPTPTPTPTPTPTPT--TPSPT--TPPTPTPTPTPTPTPTPTPTPT 471
Db 413 SRIIPREWAKPPSPSQEP-DDTPYIPTTHAPKPSRKPKPT--TTTVAATPVAT 469

Qy 472 TPTPAPTSTSPSTTTE-----HTSETP-----KYTTYVDGHLIKYKEDIPHPT 517
Db 470 -----TTTEHHHHHEEKPSQDNQVSGDQTATD---VDCSQEDYLFH-E 512
Qy 518 NIHKYLVCFVNGWGWVH-----IMPCPPGTIW 545
Db 513 DCKNYKRC-----VHGEAVLFTCREGTIVY 536
RESULT 12
US-09-545-814-14
; Sequence 14, Application US/09545814
; Patent No. 6416977
; GENERAL INFORMATION:
; APPLICANT: Becher, Anna M.
; TITLE OF INVENTION: FLEA CHITINASE NUCLEIC ACID MOLECULES, PROTEINS AND
; FILE OF INVENTION: USES THEREOF
; FILE REFERENCE: FC-S-C1
; CURRENT APPLICATION NUMBER: US/09/545,814
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/128,833
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 559
; TYPE: PRT
; ORGANISM: Ctenocephalides felis
US-09-545-814-14
Query Match 26.1%; Score 811.5; DB 4; Length 559;
Best Local Similarity 35.8%; Pred. No. 7.1e-57;
Matches 193; Conservative 86; Mismatches 193; Indels 71; Gaps 22;
Qy 34 RIVCVGTWVYHK-VDPYTIEDIDPFKTHLMYGFAKIDYKTYIQVDFPYQDDNHNWS 92
Db 5 RIVCFPSNWAYRPGICRYGIEDIPVLCITHIVSYGIVDDKDSVLVIDPELDIDNN-- 62
Qy 93 EKGYERFNNRLKNPBLTMTISLGGWYEGSEKYSMDAANPTYRQFIQSVDLFLQBYK 152
Db 63 ---GFKNFTNLRKIHNPVQLQIAGVWAGGKYSYTWAEKRKRSAFIRSVDFMNEYKF 119
Qy 153 DGLDLWEYFGSR-LGNPKDKQNYLALVRELKDAFEPHG--YLLTAASVSPGDKIDRAY 209
Db 120 DGFPLDWEYFGAARDGGSFSDKCKFLYFVQELRAFNKQKQWEITMAVFIARFLQEGY 179
Qy 210 DIKELNKLFDWMNVMTYDVGWENFYGHNAPLYKRPDETDLHTYFNVTMHHYLNNG 269
Db 180 HVPCLCELLDAIHVMSYDLRGNWAGFADTHSPLYRRPHD-QYAYEKLNVNDGQLWDMG 238
Qy 270 ATRDKLVMGVFPFGRAWSIEDRSK-LKLG---DPAKMSPPGFSIGBEGVLSYIELCOLF 325
Db 239 CPANKLVGVFPFGRSFTLSNSKDYELGTYNKEAGGEPGYTNATGFSIYEICLEV 298
Qy 326 Q--KEEMHIQYDEYNAPYNDKINWGYDDLASISCKLAFKELGVSGVMVMSLENDPF 383
Db 299 DDPKSGKWTXKDEHGKVPYAYKGNQWGYEDPKSVALKMEFIKSKGVGGAWTWAIMDDF 358
Qy 384 KHCGC-PKNPLLNKVNHMINGDEKNSFECILGSTTTPP--TTTTTPTTTTTPSTPT 440
Db 359 QGVCSDDKHTLAVIMHDYM---KNYIVPFDSRITPRPEWAKPSPSTPSQEP-DDTPYI 413
Qy 441 PTT-TPSPPT-TPPTTSPPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTT 493
Db 414 PTTTHAPKSPKPTKPKPT--TTTVAATTVPAT-----TTTEHHHHHEEEK 458
Qy 494 P-----KYTTYVDGHLIKYKEDIPHPTNIHKYLVCFVNGWGWVH-----IMPCP 540
Db 459 PSEQDNQVSGDQTATD---VDCSQEDYLFH-EDCKNYKRC-----VHGEAVLFTCR 506
Qy 541 PGTIW 545
Db 507 EGTIV 511

RESULT 13
US-08-486-839-4
; Sequence 4, Application US/08486839
; Patent No. 5928928
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: A human chitinase, its recombinant
; TITLE OF INVENTION: production, its use for decomposing chitin, its use
; TITLE OF INVENTION: in therapy or prophylaxis against infection diseases.
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Hoffmann & Baron
; STREET: 350 Jericho Turupike
; CITY: Jericho
; STATE: New York
; COUNTRY: United States of America
; ZIP: 11758
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; SOFTWARE:
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,839
; FILING DATE: 07 - June - 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Baron, Ronald J.
; REGISTRATION NUMBER: 29,281
; REFERENCE/DOCKET NUMBER: 294-26
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 822-3550
; TELEFAX: (516) 822-3582
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 466 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-486-839-4
Query Match 23.8%; Score 738; DB 2; Length 466;
Best Local Similarity 34.2%; Pred. No. 4.3e-51;
Matches 152; Conservative 85; Mismatches 150; Indels 58; Gaps 11;
Qy 34 RIVCVGTWVYHKVDP-YTIEDIDPFKTHLMYGFAKIDYKTYIQVDFPYQDDNHNWS 92
Db 23 KLVCFYTNWAOYRQGEARFLPKDLDPCLTHLYAFAGTWNHQLST-----TEW 71
Qy 93 -EKGYERFNNRLKNPBLTMTISLGGWYEGSEKYSMDAANPTYRQFIQSVDLFLQBYK 151
Db 72 NDETLYQBFNGLKQNNPKLTLLAIGWNFGTQKFTDMVATANNRQTFVNSAIRFLKYS 131
Qy 152 DGLDLWEYFGSR-LGNPKDKQNYLALVRELKDAFEPHG-----YLLTAASVSPGDK 204
Db 132 DGLDLWEYFGSQ-GSPAVDKERFTTLVQDLANAFQQAQTSKGERLLLSAFAVAGQY 190
Qy 205 IDRAYDIKELNKLFDWMNVMTYDVGWENFYGHNAPLYKRPDETDLHTYFNVTMHHY 264
Db 191 VDAGYEVKIAQLNDFVNLMAIDFHSWEKVTGHNPSPLYKQESGSAAS-LNVDAVQQ 249
Qy 265 YLNGATRDKLVMGVFPFGRAWSIEDRSKILKGLDPAKMSPPGFTSGBEGVLSYIELCOL 324
Db 250 WLQKGTASKLILGMPYTGSRFTLASSSDTRVGAATGSGTGPFTKEGMLAYEVCWS 309
Qy 325 FQKEWHIYDEYNAPYNDKINWGYDDLASISCKLAFKELGVSGVMVMSLENDPFK 384
Db 310 KGATKQRIQ-DQ--KVPYIFRDNQWVGDDVBSFRTKYSYLKQKGLGGAMWALDDFA 366

Db	191	VDAGYEVDKIAQNLDVFNLMAYDFHGSWEKVTGHSPLYKROESGAAS-LNVDAAVQQ	249
QY	265	YLNNGATRDKLVNGVFPYGRAMSIEDRSKILGDPKAGMSPFGFISGEEGLSYIELCOL	324
Db	250	WLQKGTTPASKLILGMFTYGRSFTLASSSDTRVGAPATGSGTGPFTKEGMLAYEVCWS	309
QY	325	FOKEWHIQYDEYNAPYGYNDKIWVGYYDDLASISCKLAFKLGVSGVMWSLENDDEPK	384
Db	310	KGATKQRIQ-DQ--KVEYIFRDNQWYGFDDVESFKTKVSYLKQGLGGAMWALDLDFA	366
QY	385	GHCGPKNPLLNKVHNMINGDEKNSFECILGSPSTTTTPTTTTPTTTTPTTTTPTTTT	444
Db	367	G-----FSCNQ-----RYPLIQTLROELSILPLPSGT	394
QY	445	PSPTTTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPT	469
Db	395	PELEVP-KPGQPSEPEHGPSPGQDT	418

Search completed: March 22, 2004, 07:04:00
Job time : 46.7332 secs